

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 03:18:36 ; Search time 1761 Seconds

(without alignments)
1238.208 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MMIFCQKQKINVRKNSNGE.....IRIYNTRAKKINTCNCYP 45

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgm2_1/USPRO_epool_p/US10614934/runat_17082005_181356_22080/app.query.fasta_1.199
-DB=genemb1 -QMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10614934 @CGN 1.1 5600 @runat_17082005_181356_22080 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=150 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ars:*
12: gb_ay:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	100.0	138	6	AR359345
2	102	38.3	151	12	SYNCTX
3	101	38.0	114	6	AR359343
4	92.5	34.8	186	6	AX063238

5	91.5	34.4	154	6	118309
6	91.5	34.0	254	3	AAU427744
7	90.5	34.0	254	3	AAU427743
8	90	33.8	323	3	AY225782
9	88	33.1	288	3	AF151537
10	88	33.1	348	3	AF247058
11	88	33.1	372	3	AF208300
12	87.5	32.9	180	6	AX063240
13	86.5	32.5	120	6	118306
14	86.5	32.5	174	6	AX063254
15	86.5	32.5	263	3	AAU427745
16	83.5	31.4	313	3	AF079062
17	83.5	31.4	400	3	AF208298
18	82	30.8	160	3	PIU79579
19	79.5	29.9	300	3	AF153692
20	79.5	29.9	190371	2	AC116830
21	78.5	29.5	281	3	AF541980
22	78	29.3	180	6	AR359346
23	77.5	29.1	293	3	AY156725
24	77	28.9	150	6	AR359344
25	76.5	28.8	379	3	AF208299
26	75	28.2	176	6	AX063250
27	75	28.2	181329	2	BX569779
28	73	27.4	177	6	AR359339
29	73	27.4	312	3	AY225783
30	72.5	27.3	11000	2	AC098036-2
31	72.5	27.3	213887	2	AC128587
32	72.5	27.3	239732	2	AC098491
33	72.5	27.3	322972	2	AC129853
34	72	27.1	4674	3	PTG11A2
35	72	27.1	36596	2	AC149403
36	72	27.1	151441	2	AC149687
37	72	27.1	238844	2	AC097683
38	71.5	26.9	272	3	S74733
39	71.5	26.9	183629	2	CR847835
40	71.5	26.9	185257	5	AL929568
41	71.5	26.9	209810	2	AC106935
42	71.5	26.9	214878	2	CR846099
43	71	26.7	177	6	AX063252
44	71	26.7	144641	2	AC116530
45	71	26.7	146202	10	AL928553

ALIGNMENTS

RESULT 1
AR359345
LOCUS AR359345 138 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6593141.
ACCESSION AR359345
VERSION AR359345.1 GI:33765592
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 138)
AUTHORS Herman,R., Wong,J.F., Lu,A.L., Presnail,J.K. and Lee,J.-M.
TITLE Scorpion toxins
JOURNAL Patent: US 6593141-A 13 15-JUL-2003;
FEATURES
source location/Qualifiers
1..138
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 6.62e-26 Length: 138
Score: 266.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

```

US-10-614-934-14 (1-45) x AR359345 (1-138)
QY 1 MetMetIlePheCySGInGlyGlnIysIleAsnTYrArgCysAsnAsnSerGlyGlu 20
DB 1 ATGATGATTTTCTGCAAGCCAGAAAAATAATTTCATGTATTAATAGCGGTGAG 60
QY 21 CysIleProHisCysIleArgIleTYrAsnThrArgAlaIalysCysIleAsnIleThr 40
DB 61 TGAATTCACATTCATCAAGAAATATATACACAGAGACGAAAGTATTAATAAACA 120
QY 41 CysAsnCySTyrPro 45
DB 121 TGCATTTGTTATCCA 135

RESULT 2
SYNCTX 151 bp DNA linear SYN 27-APR-1993
LOCUS Synthetic scorpion charybdotoxin gene,3' end.
DEFINITION M64610.1 GI:208160
ACCESSION M64610
VERSION M64610.1 GI:208160
KEYWORDS charybdotoxin; peptide blocker of K+ channels.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 151)
AUTHORS Park,C.S., Hausdorff,S.F. and Miller,C.
TITLE Design, synthesis, and functional expression of a gene for
JOURNAL charybdotoxin, a peptide blocker of K+ channels
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2046-2050 (1991)
PUBMED 91172749
COMMENT 1706515
FEATURES
source Original
location/Qualifiers
1..151
/mol_type="synthetic construct"
/db_xref="taxon:32630"
1..138
/gene="CTX"
<1..138
/gene="CTX"
/codon_start=1
/transl_table=1
/product="charybdotoxin"
/protein_id="AA073014.1"
/db_xref="GI:208161"
/translation="VDSIEGRQPTNVSCTTSKECWGVQRLHNTSRGKGMKKRCRY
S"

ORIGIN
Alignment Scores:
Pred. No.: 0.000188 Length: 151
Score: 102.00 Matches: 17
Percent Similarity: 58.97% Conservative: 6
Best Local Similarity: 43.59% Mismatches: 16
Query Match: 38.35% Indels: 0
DB: 12 Gaps: 0

US-10-614-934-14 (1-45) x SYNCTX (1-151)
QY 6 GlnGlyGlnIysIleAsnTYrArgCysAsnAsnSerGlyGluCysIleProHisCys 25
DB 16 GAAGGTGCTCAATTTACCAATGTTCTTGTAACAATTAAGAAATGTGGTCCGTTGT 75
QY 26 IleArgIleTYrAsnThrArgAlaIalysCysIleAsnIleThrCysAsnCySTyr 44
DB 76 CAACGTCTGCATTAACACAGCCGCGGTAAATGCAATGAACAAAAATGTCGTTGTA 132

RESULT 3
LOCUS AR359343
DEFINITION Sequence 9 from patent US 6593141.
ACCESSION AR359343
114 bp DNA linear PAT 17-AUG-2003

```

```

VERSION AR359343.1 GI:33765590
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 114)
AUTHORS Herman,R., Wong,J.F., Lu,A.L., Prensall,J.K. and Lee,J.-M.
TITLE Scorpion toxins
JOURNAL Patent: US 6593141-A 9 15-JUL-2003;
FEATURES
source location/Qualifiers
1..114
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0.00019 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: 6 Gaps: 0

US-10-614-934-14 (1-45) x AR359343 (1-114)
QY 12 AsnTYrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTYrAsnThr 31
DB 10 AATGTGCGCGTCAAGCAATTCGGAACAATGTCGTCAGTTTGCAATAAAGATAAATAT 69
QY 32 ArgAlaIalysCysIleAsnIleTYrAsnCySTyrPro 45
DB 70 AATGCGGAAGTGTGTAATGACAAATGATTTGTTATCCA 111

RESULT 4
LOCUS AX063238
DEFINITION Sequence 3 from Patent WO0078958.
ACCESSION AX063238
VERSION AX063238.1 GI:12541063
KEYWORDS
SOURCE Hottentotta judaica
ORGANISM Hottentotta judaica
REFERENCE 1
AUTHORS Hermann,R., Lee,J.M. and Wong,J.F.
TITLE Scorpion toxins from buthous judaicus
JOURNAL Patent: WO 0078958-A 3 28-DEC-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
source location/Qualifiers
1..186
/organism="Hottentotta judaica"
/mol_type="unassigned DNA"
/db_xref="taxon:6863"

ORIGIN
Alignment Scores:
Pred. No.: 0.00407 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063238 (1-186)
QY 1 MetMetIlePheCySGInGlyGlnIysIleAsnTYrArgCys--AsnAsnSerGly 19
DB 46 ATGTTATTTTCAGACCAAGCTCAATACAGTTGATGATTAACGTATGGAGAGACAT 105
QY 20 GluCysIleProHisCysIleArgIleTYrAsnThrArgAlaIalysCysIleAsnIys 39
DB 106 AATTGCTAAACCAATGATGATTAATAGCGACCACTAAACTAAATGATCAATCAAT 165

```

Qy 40 ThrCysAenCysTyrPro 45
 |||||
 Db 166 CGGTCCACTGTATCCG 183

RESULT 5
 LOCUS 118309 154 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 5 from patent US 5494895.
 ACCESSION 118309
 VERSION 118309.1 GI:1598664
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 154)
 AUTHORS Garcia,M.L., Koo,G.C., Leonard,R.J., Lin,C.-C.S., Slaughter,R.S.,
 Stevens,S.P. and Williamson,J.M.
 TITLE Scorpion peptide margatoxin with immunosuppressant activity
 JOURNAL Parent: US 5494895-A 5 27-FEB-1996;
 FEATURES Location/Qualifiers
 source 1..154
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00452 Length: 154
 Score: 91.50 Matches: 16
 Percent Similarity: 58.54% Conservative: 8
 Best Local Similarity: 39.02% Mismatches: 16
 Query Match: 34.40% Indels: 1
 DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x 118309 (1-154)
 Qy 6 GlnGlnGlnLysLysIleAsnTyrArgCysAenAenSerGlyGluCysIleProHisCys 25
 |||||
 Db 16 GAGGTTCGTACCATATCAACCTTAATGCACCTCTCCGAACACATGCTGCCGCGTGC 75

Qy 26 IleArgIleTyrAsnThrArgAla--AlaLysCysIleAsnLysThrCysAenCysTyr 44
 |||||
 Db 76 AAGCTCAGTTCGGTCAGTCTGCTGTGCTAATGATCATGACGTAACGTAATGCAATGCTAC 135

Qy 45 Pro 45
 |||||
 Db 136 CCG 138

RESULT 6
 LOCUS AAU427744 254 bp mRNA linear INV 10-JAN-2003
 DEFINITION Androctonus australis partial mRNA for toxin AaTx2.
 ACCESSION AJ427744
 VERSION AJ427744.1 GI:27652633
 KEYWORDS toxin AaTx2.
 SOURCE Androctonus australis (Sahara scorpion)
 ORGANISM Androctonus australis
 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Butiidae; Butioidae; Butiidae; Androctonus.

REFERENCE 1
 AUTHORS Vacher,H., Alami,M., Legros,C., Possani,L.D., Bougis,P.E. and
 Martin-Baucalatre,M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 254)
 AUTHORS Martin-Baucalatre,M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Martin-Baucalatre M.F., Institut Jean Roche,
 UMR 6560 CNRS Université de la Méditerranée, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE
 FEATURES Location/Qualifiers

source 1..254
 /organism="Androctonus australis"
 /mol_type="mRNA"
 /db_xref="taxon:6858"
 /clone="pcd-3x9"
 /country="Tunisia:Beni-Khedache"
 <18..197
 /codon_start=1
 /product="toxin AaTx2"
 /protein_id="CAD20743.1"
 /db_xref="GI:27652634"
 /translation="MKFSSTILLTLTLCMSIFGNCQVETNKKCGGSCASVCRRTG
 VAAGKINRCVCYP"
 sig_peptide 18..83
 mat_peptide 84..192
 /product="toxin AaTx2"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.0076 Length: 254
 Score: 91.50 Matches: 19
 Percent Similarity: 48.89% Conservative: 3
 Best Local Similarity: 42.22% Mismatches: 22
 Query Match: 34.40% Indels: 1
 DB: 3 Gaps: 1

US-10-614-934-14 (1-45) x AAU427744 (1-254)
 Qy 1 MetMetIlePheCysGlnGlnLysIleAsnTyrArgCysAenAenSerGlyGlu 20
 |||||
 Db 63 ATGACACATCTTCGGCAATGCGCAAGTGAACCAACAGAAATGT---CAAGCTGATCG 119

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaIleLysCysIleAsnLysThr 40
 |||||
 Db 120 TGTGCTTAGTATGAGAGATATGAGATGAGTCTGCTGGCAATGATTAATGGAAGA 179

Qy 41 CysAenCysTyrPro 45
 |||||
 Db 180 TGTGCTCTACCC 194

RESULT 7
 LOCUS AAU427743 254 bp mRNA linear INV 10-JAN-2003
 DEFINITION Androctonus australis partial mRNA for toxin AaTx1.
 ACCESSION AJ427743
 VERSION AJ427743.1 GI:27652631
 KEYWORDS toxin AaTx1.
 SOURCE Androctonus australis (Sahara scorpion)
 ORGANISM Androctonus australis
 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Butiidae; Butioidae; Butiidae; Androctonus.

REFERENCE 1
 AUTHORS Vacher,H., Alami,M., Legros,C., Possani,L.D., Bougis,P.E. and
 Martin-Baucalatre,M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 254)
 AUTHORS Martin-Baucalatre,M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Martin-Baucalatre M.F., Institut Jean Roche,
 UMR 6560 CNRS Université de la Méditerranée, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE
 FEATURES Location/Qualifiers
 source 1..254
 /organism="Androctonus australis"
 /mol_type="mRNA"
 /db_xref="taxon:6858"
 /clone="pcd-3x11"
 /country="Tunisia:Beni-Khedache"
 <18..197
 /codon_start=1

```

ORIGIN
Alignment Scores:
Pred. No.: 0.0103 Length: 254
Score: 90.50 Matches: 19
Percent Similarity: 48.89% Conservative: 3
Best Local Similarity: 42.22% Mismatches: 22
Query Match: 34.02% Indels: 1
DB: 3 Gaps: 1

US-10-614-934-14 (1-45) x AAU427743 (1-254)

QY 1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 63 ATGAGCATCTTCGGCAATTGCCAATTGAAACAAACAGAAATGT---CAAGGTGATCG 119
QY 21 CysIlePheHisCysIleArgGlyLeuTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db 120 TGTGCTTCAGTATGAGAGATGATTTGAGTACTGCTGGCAATGTATTATGAGAGA 179
QY 41 CysAsnCysTyrPro 45
Db 180 TGTGCTGCTACCCC 194

RESULT 8
AY225782 323 bp mRNA linear INV 12-OCT-2003
LOCUS Opisthophthalmus carinatus potassium channel toxin KTx4 mRNA,
DEFINITION complete cds.
ACCESSION AY225782
VERSION AY225782.1 GI:37539451
KEYWORDS
SOURCE
ORGANISM
Opisthophthalmus carinatus
Opisthophthalmus carinatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Tutrida; Scorpionoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
REFERENCE
1 (bases 1 to 323)
AUTHORS Zhu,S., Isabelle,H., Dyason,K., Verdonck,F. and Tytgat,J.
TITLE Evolutionary trace analysis of scorpion toxins specific for
K-channels
JOURNAL Proteins (2003) In press
REFERENCE
2 (bases 1 to 323)
AUTHORS Zhu,S., Dyason,K., Verdonck,F. and Tytgat,J.
TITLE Scorpion alpha-K+ Channel Toxin Family: Molecular Cloning and
JOURNAL Evolutionary Prediction of Channel-Binding Sites
REFERENCE
3 (bases 1 to 323)
AUTHORS Tytgat,J., Zhu,S., Verdonck,F. and Dyason,K.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2003) Lab of Toxicology, Leuven University, E.
Van Evensterat 4, Leuven 3000, Belgium
FEATURES
source
1..323
location/Qualifiers
/organism="Opisthophthalmus carinatus"
/mol_type="mRNA"
/db_xref="taxon:190115"
/tissue_type="venom gland"
31..216
/note="CKTx4, belongs to alpha-potassium channel toxin
subfamily 6"
/codon_start=1
/product="potassium channel toxin KTx4"
/protein_id="AAP71820.1"
/db_xref="GI:37539452"
/translation="MNAKFTILLVTTTLLPDAKAGELIRSGTRECYPQCKLTG

```

```

ORIGIN
Alignment Scores:
Pred. No.: 0.0153 Length: 323
Score: 90.00 Matches: 17
Percent Similarity: 60.98% Conservative: 8
Best Local Similarity: 41.46% Mismatches: 13
Query Match: 33.83% Indels: 3
DB: 3 Gaps: 1

US-10-614-934-14 (1-45) x AY225782 (1-323)

QY 5 CysGlnGlyGlnLysIleAsnTyr-ArgCysAsnAsnSerGlyGlyCysIleProhi 24
Db 90 TGCAAGGGCGCCGCA-----AATTATCAGATGCGAAGCAAGGAGTGTATGCCCC 143
QY 24 CysIleArgGlyLeuTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
Db 144 ATGCCAAGGCTTACCGAGTGTCTTAATGCMAAATGATGAGCAAGAGCTGCAATGTTA 203
QY 44 r 44
Db 204 C 204

RESULT 9
AF151537 288 bp mRNA linear INV 18-AUG-2003
LOCUS Butus martenisi potassium channel toxin precursor (Tx2) mRNA,
DEFINITION complete cds.
ACCESSION AF151537
VERSION AF151537.1 GI:3337896
KEYWORDS
SOURCE
ORGANISM
Mesobuthus martenisi (Butus martenisi)
Mesobuthus martenisi
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butrida; Butoidea; Butidae; Mesobuthus.
REFERENCE
1 (bases 1 to 288)
AUTHORS Zeng,X.-C., Li,W.-X. and Zu,S.-Y.
TITLE The cDNA sequence encoding the precursor of toxin TX2 from the
Chinese scorpion Butus martenisi Karsch which is active on
potassium channel
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 288)
AUTHORS Li,W.-X., Zeng,X.-C. and Zu,S.-Y.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1999) Department of Virology and Molecular
Biology, Institute of Virology, Wuhan University, Luojia Street,
Wuhan, Hubei 430072, P.R. China
FEATURES
source
1..288
location/Qualifiers
/organism="Mesobuthus martenisi"
/mol_type="mRNA"
/db_xref="taxon:34649"
/tissue_type="venom gland"
/note="authorily: Butus martenisi Karsch"
1..288
/gene="Tx2"
28..204
/gene="Tx2"
/note="Tx2"
/codon_start=1
/product="potassium channel toxin precursor"
/protein_id="AAQ13576.1"
/db_xref="GI:3337897"
/translation="MKISFLLLAIVICISGWTEAQTNTVSCASGQCPVCKLFGT
YRKCKMSKRCYS"
ORIGIN

```

Alignment Scores:
 Pred. No.: 0.0248 Length: 288
 Score: 88.00 Matches: 13
 Percent Similarity: 57.58% Conservative: 6
 Best Local Similarity: 39.39% Mismatches: 14
 Query Match: 33.08% Indels: 0
 DB: 3 Gaps: 0

US-10-614-934-14 (1-45) x AF151537 (1-288)

QY 12 AenTYrARgCYsAsnAsnSerGlyGlyCysIleProHIScysIleArgIleTyraSnThr 31
 ||| |||::: |||::: ||| ||| |||::: |||
 DB 100 AATGAAAGTTGAGAGCATCTAGTGAATGTTGCCCGTTTGAATAAAGTTGTTGAAACG 159
 ||| |||::: |||::: ||| ||| |||::: |||

QY 32 ArgAlaAlaIalYcysIleAsnLysThrCYsAsnCYsTYr 44
 ||| |||::: |||::: ||| ||| |||::: |||
 DB 160 TACAGGGGAAAATGTATGTATGTAAGAAAGCCGTTGTAT 198
 ||| |||::: |||::: ||| ||| |||::: |||

RESULT 10
 AF247058 348 bp DNA linear INV 18-JUL-2001
 LOCUS Butus martensii potassium channel toxin Bmtx2 gene, complete cds.
 ACCESSION AF247058
 VERSION AF247058.1 GI:14794951
 KEYWORDS Mesobuthus martensii (Butus martensii)
 SOURCE Mesobuthus martensii
 ORGANISM Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Butrida; Butioidae; Butridae; Mesobutha.
 REFERENCE 1 (bases 1 to 348)
 Zeng,X.-C., Zhu,Z.-H., Li,W.-X., Zhu,S.-Y., Peng,F., Mao,X. and Liu,H.
 TITLE Molecular cloning and genomic organization of a K(+) channel toxin from the Chinese scorpion Butus martensii Karsch
 JOURNAL Toxicon 39 (2-3), 407-410 (2001)
 MEDLINE 20436245
 PUBMED 10978761
 REFERENCE 2 (bases 1 to 348)
 Li,W.-X., Zhu,Z.-H., Zeng,X.-C., Peng,F., Mao,X. and Liu,H.
 AUTHORS Direct Submission
 JOURNAL Submitted (19-MAR-2000) Biotechnology, Virology, Wuja, Wuhan, Hubei 430072, P. R. China
 FEATURES
 source
 1..348
 location/Qualifiers
 /organism="Mesobuthus martensii"
 /mol_type="genomic DNA"
 /db_xref="taxon:34649"
 /clone="100"
 join(<22..70,152..279)
 /product="potassium channel toxin Bmtx2"
 join(<22..70,152..279)
 /note="acts on voltage-gated and high-conductance Ca++-activated K+ channels"
 /codon_start=1
 /product="potassium channel toxin Bmtx2"
 /protein_id="AAK7518.1"
 /db_xref="GI:14794952"
 /translation="WKISFLLILAVICISGTEAQFNVSCASASQCPVCKKLFGFGRKCMKRCRCYS"
 YRGKCMKRCRCYS"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.0302 Length: 348
 Score: 88.00 Matches: 13
 Percent Similarity: 57.58% Conservative: 6
 Best Local Similarity: 39.39% Mismatches: 14
 Query Match: 33.08% Indels: 0
 DB: 3 Gaps: 0

US-10-614-934-14 (1-45) x AF247058 (1-348)

QY 12 AenTYrARgCYsAsnAsnSerGlyGlyCysIleProHIScysIleArgIleTyraSnThr 31
 ||| |||::: |||::: ||| ||| |||::: |||
 |||::: |||::: ||| ||| |||::: |||

Db 175 AATGTAAGTGGACAGTGCATCTAGTCATCATGTGTCGGCGGTTTGTAATAAAGTTGTTGGAACG 234

Qy 32 ArgAlaAlaLysCysIleAenLysThrCysAsnCysTyr 44
 |||||
 |||||

Db 235 TACAGGGGAAAATGTATGAAATAGTAATGCGCGTTGTTAT 273

RESULT 11

LOCUS AF208300 372 bp DNA linear INV 20-APR-2000

DEFINITION Butus martenisi neurotoxin TX2 (TX2) gene, complete cds.

ACCESSION AF208300

VERSION AF208300.1 GI:7576750

KEYWORDS

SOURCE

ORGANISM

Mesobuthus martenisi (Butus martenisi)

Mesobuthus martenisi

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Butida; Butioidae; Butidae; Mesobuthus.

1 (bases 1 to 372)

Da,L., Wu,J.J., Gu,Y.H., Lan,Z.D., Ling,M.H. and Chl,C.W.
 Genomic organization of three novel toxins from the scorpion Butus martenisi Karsch that are active on potassium channels
 Biochem. J. 346 Pt 3, 805-809 (2000)

2 (bases 1 to 372)

Da,L., Wu,J.J., Gu,Y.H., Lan,Z.D. and Chl,C.W.
 Direct Submission
 Submitted (26-NOV-1999) State Key Laboratory of Molecular Biology,
 Shanghai Institute of Biochemistry, Chinese Academy of Sciences,
 320 Yueyang Road, Shanghai 200031, China

Location/Qualifiers

1..372

/organism="Mesobuthus martenisi"

/mol_type="genomic DNA"

/db_xref="taxon:34649"

/note="nauthority: Butus martenisi Karsch; synonym: Butus martenisi; common: scorpion"

1..372

/gene="TX2"

/note="BmTX2"

join(1..95,176..372)

/gene="TX2"

/product="neurotoxin TX2"

1..46

/gene="TX2"

join(47..95,176..303)

/gene="TX2"

/codon_start=1

/product="neurotoxin TX2"

/protein_id="AA063972.1"

/db_xref="GI:7576751"

/translation="MKISFLLLAIVCSIGWTEAQTNVNSCASQCPVCKKLTGT
 YRCKNMSKRCRCS"

join(47..95,176..189)

/gene="TX2"

304..372

/gene="TX2"

ORIGIN

Alignment Scores:

Pred. NO.: 0.0324 Length: 372

Score: 88.00 Matches: 13

Percent Similarity: 57.58% Conservative: 6

Best Local Similarity: 39.39% Mismatches: 14

Query Match: 33.08% Indels: 0

DB: 3 Gaps: 0

US-10-614-934-14 (1-45) x AF208300 (1-372)

Qy 12 AsnTyrArgCysAsnAenSergLysCysIleProHisCysIleArgIleTyrAsnThr 31
 |||||
 |||||

Db 199 AATTAAGTGGACAGTGCATCTAGTCATCATGTGTCGGCGGTTTGTAATAAAGTTGTTGGAACG 258

```

Qy      32 ArgAlaAlaIyGySIIeAsnIyThrCySaSnCySTyr 44
Db      259 TACAGGGGAAATGTATGAATGTAATAATGCGGTGTAT 297

RESULT 12
AX063240
LOCUS      AX063240             180 bp      DNA      linear      PAT 24-JAN-2001
DEFINITION Sequence 5 from Patent WO0078958.
ACCESSION  AX063240
VERSION     AX063240.1  GI:12541064
KEYWORDS
SOURCE      Hottentotta judaica
            Hottentotta judaica
            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
            Butrida; Buthoidea; Butridae; Hottentotta.

REFERENCE
  1 Herrmann, R., Lee, J.M. and Wong, J.F.
    Scorpion toxins from buthous judaicus
    Patent: WO 0078958-A 5 28-DEC-2000;
    JOURNAL  E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
  source
    /organism="Hotentotta judaica"
    /mol_type="unassigned DNA"
    /db_xref="taxon:6863"

ORIGIN
Alignment Scores:
Pred. No.:      0.0177      Length:      180
Score:          87.50      Matches:      18
Percent Similarity: 46.67%      Conservative: 3
Best Local Similarity: 40.00%      Mismatches: 23
Query Match:    32.89%      Indels:      1
DB:             6          Gaps:          1

US-10-614-934-14 (1-45) x AX063240 (1-180)

Qy      1 MetMetIlePheCySGInGlyGlnIyLeAsnTyRArgCySaSnSergIyGlu 20
Db      46 ATGACCATATGATTAATTGCAAGTAAGAAACAATGCAATGT---ACAGTGCGCTCA 102

Qy      21 CysIleProHisCySIIeArgIleTyRAsnThrArgAlaAlaIyGySIIeAsnIyThr 40
Db      103 TGTCTTCACATGTAAGAGTAATAGAGTACCTGACGAGAAATGCATTAAATGAAGA 162

Qy      41 CysAsnCySTyrPro 45
Db      163 TGTGTCTGCTATCCG 177

RESULT 13
I18306
LOCUS      I18306             120 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 2 from patent US 5494895.
ACCESSION  I18306
VERSION     I18306.1  GI:1598661
KEYWORDS
SOURCE      Unknown.
            Unclassified.
REFERENCE
  1 (bases 1 to 120)
  Garcia, M.L., Koo, G.C., Leonard, R.J., Lin, C.-C.S., Slaughter, R.S.,
  Stevens, S.P. and Williamson, J.M.
  Scorpion peptide margatoxin with immunosuppressant activity
  Patent: US 5494895-A 2 27-FEB-1996;
  JOURNAL
FEATURES
  source
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      0.0157      Length:      120
Score:          86.50      Matches:      15

```

```

Percent Similarity: 58.33%      Conservative: 6
Best Local Similarity: 41.67%      Mismatches: 14
Query Match:      32.52%      Indels:      1
DB:             6          Gaps:          1

US-10-614-934-14 (1-45) x I18306 (1-120)

Qy      11 IleAsnTyRArgCySaSnAsnSergIyGlnCySIIeProHisCySIIeArgIleTyRAsn 30
Db      7 ATCAACGTTAAATGACACCTCTCCGAAACAGTGCCTGCCGCGCAAGTCAGTCCGT 66

Qy      31 ThrArgAla---AlaIyGySIIeAsnIyThrCySaSnCySTyrPro 45
Db      67 CAGTCTGCTGATGCTAATATGATGAACGTTAAATGCAAAATGTAACCG 114

RESULT 14
AX063254
LOCUS      AX063254             174 bp      DNA      linear      PAT 24-JAN-2001
DEFINITION Sequence 19 from Patent WO0078958.
ACCESSION  AX063254
VERSION     AX063254.1  GI:12541071
KEYWORDS
SOURCE      Hottentotta judaica
            Hottentotta judaica
            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
            Butrida; Buthoidea; Butridae; Hottentotta.

REFERENCE
  1 Herrmann, R., Lee, J.M. and Wong, J.F.
    Scorpion toxins from buthous judaicus
    Patent: WO 0078958-A 19 28-DEC-2000;
    JOURNAL  E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
  source
    /organism="Hotentotta judaica"
    /mol_type="unassigned DNA"
    /db_xref="taxon:6863"

ORIGIN
  unsure
  unsure
  88

Alignment Scores:
Pred. No.:      0.0231      Length:      174
Score:          86.50      Matches:      17
Percent Similarity: 52.27%      Conservative: 6
Best Local Similarity: 38.64%      Mismatches: 20
Query Match:    32.52%      Indels:      1
DB:             6          Gaps:          1

US-10-614-934-14 (1-45) x AX063254 (1-174)

Qy      1 MetMetIlePheCySGInGlyGlnIyLeAsnTyRArgCySaSnAsnSergIyGlu 20
Db      40 ATATATGATTTCAACCGAAGCTCAG---TTATATGACGTGAATGCACATCANTTAAGGAA 96

Qy      21 CysIleProHisCySIIeArgIleTyRAsnThrArgAlaAlaIyGySIIeAsnIyThr 40
Db      97 TGTGGCGCTATTGTTAGAGAAAGATTGTGTGCGCAGAGAAAGTGCATTAATAACAA 156

Qy      41 CysAsnCySTyr 44
Db      157 TGCCGTGTGTAT 168

RESULT 15
AAU427745
LOCUS      AAU427745             263 bp      DNA      linear      INV 10-JAN-2003
DEFINITION Androctonus australis tx1 gene for toxin AaTx1, exons 1-2.
ACCESSION  AAU427745
VERSION     AAU427745.1  GI:27652635
KEYWORDS
SOURCE      Androctonus australis
            Androctonus australis (Sahara scorpion)
            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
            Butrida; Buthoidea; Butridae; Androctonus.

```

REFERENCE 1
 Vacher, H., Alami, M., Legros, C., Possani, L.D., Bougis, P.E. and

AUTHORS Martin-Eaucalade, M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from

venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterisation and gene structure

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 263)
 AUTHORS Martin-Eaucalade, M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Martin-Eaucalade M.F., Université de la

Méditerranée, Institut Jean Roche UMR 6560 CNRS, Bd Pierre Dramard,
 F-13916 Marseille cedex 20, FRANCE

FEATURES
 source 1..263
 location/Qualifiers

/organism="Androctonus australis"

/mol_type="genomic DNA"

/db_xref="taxon:6858"

/tissue_type="muscle"

/country="Tunisia:Beni-Khadache"

1..263

/gene="tx1"

join(1..66,133..263)

/gene="tx1"

1..66

/gene="tx1"

/number=1

join(18..66,133..263)

/gene="tx1"

/codon_start=1

/product="toxin AaTx1"

/protein_id="CAD20744.1"

/db_xref="GI:27652636"

/translation="MKFSSILLTLICMSLFGNCQLEFNKKCGSSCASVCRVIG

VAAKCIINGRCVCYP"

join(18..66,133..149)

/gene="tx1"

150..260

/gene="tx1"

/product="toxin AaTx1"

67..132

/gene="tx1"

/number=1

133..263

/gene="tx1"

/number=2

exon

intron

sig_peptide

mat_peptide

ORIGIN

Alignment Scores:

Pred. No.:	0.0354	Length:	263
Score:	86.50	Matches:	18
Percent Similarity:	48.84%	Conservative:	3
Best Local Similarity:	41.86%	Mismatches:	21
Query Match:	32.52%	Indels:	1
DB:	3	Gaps:	1

US-10-614-934-14 (1-45) x AAU427745 (1-263)

QY 3 IIEphecysGInGlyGlnLysleleAanTyraGysaAaenSerGlyGlnCysIle 22
 Db 135 ATCTTCGGCAATTCGCCAATTCGAACAAGAAATGT---CAAGTGGATCGTGTCT 191
 QY 23 ProHisCysIleAArgIleTyraAnThrArgAlaAlaLysCysIleAanLysThrCysAa 42
 Db 192 TCAGTATGTAGAGAGATGAGTACGTGCTGCAAAATGATTAATGAAGATGTCT 251
 QY 43 CysTyPro 45
 Db 252 TGCTACCCC 260

Search completed: August 19, 2005, 05:41:25
 Job time : 1765 secs

this Page Blank (uspto)


```

XX  Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
PI  WPI: 2000-422976/36.
DR  P-PSDB: AAY99579.
XX
XX  New nucleic acid fragment encoding a scorpion toxin that is a potassium
PT  channel agonist, useful for creating transgenic plants that are more
XX  insect-tolerant.
XX
PS  Claim 2; Page 41; 44pp; English.
XX
XX  The present sequence encodes the scorpion potassium channel agonist
CC  Charybotoxin. The toxin forms a compact structure kept rigid by three
CC  disulphide bonds. Potassium channels modulate a number of cellular events
CC  such as muscle contraction, neuro-endocrine secretion, frequency and
CC  duration of action potentials, electrolyte homeostasis and resting
CC  membrane potential. The agonist has a high affinity for the channel and
CC  may therefore act by producing an irreversible blockade of the channel.
CC  The nucleotide sequence was isolated from clone 1st.pK0016.c8.f of a cDNA
CC  library representing mRNAs from Leiurus scorpion telson tissues. The toxin
CC  is insecticidal and the cDNA sequence can therefore be used to create
CC  transgenic plants that express the toxin as a means of insect pest
CC  control. The amino acid sequence of the present toxin shows homology to
CC  the Charybotoxin artificial sequence (AAY99587)
XX
SQ  Sequence 138 BP; 55 A; 21 C; 24 G; 38 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          7.83e-27          Length:          138
Score:             266.00             Matches:          45
Percent Similarity: 100.00%           Conservative:     0
Best Local Similarity: 100.00%        Mismatches:      0
Query Match:       100.00%           Indels:          0
DB:                3                 Gaps:            0

US-10-614-934-14 (1-45) x AAA48436 (1-138)
QY  1 MetMetIlePheCySGInGlyGlnLysIleAsnTYrArgCYsAsnAsnSerGlyGlu 20
Db  1 ATGATGAAATTTCTGCGCAAGCGCAGAAAAAATAATTAATTCATGTAATAAAGCGGTGAG 60
QY  21 CysIleProHisCYsIleArgIleTYrAsnThrArgAlaAlaLysCYsIleAsnLysThr 40
Db  61 TGTATTCACATGTCATCAGATATATTAACACACAGACAGCAAGTGTATTAATAAAAAACA 120
QY  41 CysAsnCYsTYrPro 45
Db  121 TGCAAATGTTATCCA 135

RESULT 2
AAA48434
ID  AAA48434 standard; cDNA; 114 BP.
XX
AC  AAA48434;
XX
DT  15-SEP-2000 (first entry)
XX
DE  Scorpion potassium channel agonist Tityustoxin k Alpha cDNA.
XX
KW  Scorpion; tityustoxin k alpha; potassium channel agonist; insecticidal;
XX  insect-tolerant transgenic plant; ss.
XX
OS  Leiurus quinquestratus.
XX
FH  Key Location/Qualifiers
FT  CDS 1..114
FT  CDS /*tag= a
FT  CDS /partial
FT  CDS /product= "Tityustoxin k Alpha"
XX
XX  WO200032777-A2.

```

```

PD  08-JUN-2000.
XX
XX  01-DEC-1999; 99WO-US028351.
XX
XX  02-DEC-1998; 98US-0110590P.
XX
XX  (DUP) DU PONT DE NEMOURS & CO E I.
XX
XX  Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
PI  WPI: 2000-422976/36.
DR  P-PSDB: AAY99577.
XX
XX  New nucleic acid fragment encoding a scorpion toxin that is a potassium
PT  channel agonist, useful for creating transgenic plants that are more
XX  insect-tolerant.
XX
PS  Claim 2; Page 41; 44pp; English.
XX
XX  The present sequence encodes the scorpion potassium channel agonist
CC  Tityustoxin k Alpha. The toxin forms a compact structure kept rigid by
CC  three disulphide bonds. Potassium channels modulate a number of cellular
CC  events such as muscle contraction, neuro-endocrine secretion, frequency
CC  and duration of action potentials, electrolyte homeostasis and resting
CC  membrane potential. The agonist has a high affinity for the channel and
CC  may therefore act by producing an irreversible blockade of the channel.
CC  The nucleotide sequence was isolated from clone 1st.pK0015.d2.f of a cDNA
CC  library representing mRNAs from Leiurus scorpion telson tissues. The toxin
CC  is insecticidal and the cDNA sequence can therefore be used to create
CC  transgenic plants that express the toxin as a means of insect pest
CC  control. The amino acid sequence of the present toxin shows homology to
CC  the sequence of tityustoxin k alpha from Tityus serrulatus (AAY99585)
XX
SQ  Sequence 114 BP; 44 A; 15 C; 23 G; 32 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          6.55e-05          Length:          114
Score:             101.00             Matches:          17
Percent Similarity: 58.82%           Conservative:     3
Best Local Similarity: 50.00%        Mismatches:     14
Query Match:       37.97%           Indels:          0
DB:                3                 Gaps:            0

US-10-614-934-14 (1-45) x AAA48434 (1-114)
QY  12 AsnTYrArgCYsAsnAsnSerGlyGluCYsIleProHisCYsIleArgIleTYrAsnThr 31
Db  10 AATGTGCCGTGCAAGAAATTTCTGGACATATGTCGTCACATTTGCAATAAAGATTAAT 69
QY  32 ArgAlaAlaLysCYsIleAsnLysThrCYsAsnCYsTYrPro 45
Db  70 AATAGCGGGAAGTGTGTATGACAAATGATATTGTTATCA 111

RESULT 3
AAF27524
ID  AAF27524 standard; DNA; 186 BP.
XX
AC  AAF27524;
XX
DT  28-MAR-2001 (first entry)
XX
DE  Scorpion kallotoxin 2 precursor DNA.
XX
KW  Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
XX
OS  Hottentotta judaica.
XX
FH  Key Location/Qualifiers
FT  CDS 1..114
FT  CDS /*tag= a
FT  CDS /partial
FT  CDS /product= "Tityustoxin k Alpha"
XX
XX  21-JUN-2000; 2000WO-US017049.

```

PR 22-JUN-1999; 99US-0140227P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 PI WPI; 2001-071394/08.
 XX
 DR New polynucleotides encoding scorpion venom potassium-channel agonist
 PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 XX Claim 1; Page 44; 50pp; English.
 XX
 CC The present invention relates to scorpion toxins. The invention may be
 CC used for the creation of transgenic plants which express K-channel
 CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock
 XX
 SQ Sequence 186 BP; 62 A; 31 C; 37 G; 56 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00166 Length: 186
 Score: 92.50 Matches: 17
 Percent Similarity: 50.00% Conservative: 6
 Best Local Similarity: 36.96% Mismatches: 22
 Query Match: 34.77% Indels: 1
 DB: Gaps: 1
 US-10-614-934-14 (1-45) x AAF27524 (1-186)
 QY 1 MetNectIlePheCysGlnGlyGlnLysLysIleAsnTYrArgCys---AsnAsnSergIy 19
 Db 46 ATGGTATTTCGAGCCACGCTCAATACGATGGATGTAACCTGTATGCGAGACAGAT 105
 QY 20 GluCySilleProHisCysIleArgIleTYrAsnThrArgAlaAlaLysCysIleAsnLys 39
 Db 106 AATTGCGTAAACCACTGCTATGATTAATACGCGCACTAAACTTAATGCAATCAAGAT 165
 QY 40 ThrCySAsnCySlyrPro 45
 Db 166 CGGTCCAACTGTATCCG 183
 RESULT 4
 ID AAO84347 standard; cDNA; 154 BP.
 XX
 AC AAO84347;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-AUG-1995 (first entry)
 XX
 DE Synthetic gene for the expression of Margatoxin gene in E. coli.
 XX
 KW Scorpion venom; Centruroides margaritatus; margatoxin; MgTX;
 KW Synthetic gene; oligo; ss.
 XX
 OS Synthetic.
 OS
 PN WO9503065-A1.
 PD 02-FEB-1995.
 PD
 PF 19-JUL-1994; 94WO-US008063.
 PF
 PR 22-JUL-1993; 93US-00096942.
 PR
 PA (MERI) MERCK & CO INC.
 PA
 PI Garcia ML, Koo GC, Leonard RJ, Lin C, Slaughter RS, Stevens SP;

PI Williamson JM;
 XX
 DR WPI; 1995-075021/10.
 XX
 PT New purified scorpion venom peptide, Margatoxin - useful as a potent and
 PT selective inhibitor of a voltage-dependent potassium channel as an
 PT immunosuppressant.
 XX
 XX Claim 15; Page 22; 42pp; English.
 XX
 CC Margatoxin (MgTX) is purified to homogeneity from venom of the scorpion
 CC C. margaritatus. The gene encoding MgTX is constructed and this gene is
 CC expressed in E. coli to produce recombinant MgTX. The MgTX gene was
 CC constructed using two synthetic oligos. The oligos are identical to
 CC AAO84345 & AAO84346 except for the 5 dCTP bases that were added to the
 CC 5' end of each to facilitate cutting with restriction enzymes. The two
 CC oligo sequences were combined to produce the gene having the coding
 CC strand on AAO84347. Codon usage was optimised for high level expression
 CC in E. coli. It includes SalI, Factor Xa, MgTX, and Hind III. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 154 BP; 41 A; 42 C; 37 G; 34 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00178 Length: 154
 Score: 91.50 Matches: 16
 Percent Similarity: 58.54% Conservative: 8
 Best Local Similarity: 39.02% Mismatches: 16
 Query Match: 34.40% Indels: 1
 DB: Gaps: 1
 US-10-614-934-14 (1-45) x AAO84347 (1-154)
 QY 6 GlnGlyGlnLysLysIleAsnTYrArgCysAsnAsnSergIyGluCySilleProHisCys 25
 Db 16 GAAGTCTGTAACATCATCAACGTTAAATGCACCTCTCCGAACAGATGCTCGCGCGTGC 75
 QY 26 IleArgIleTYrAsnThrArgAla---AlaLysCysIleAsnLysThrCySAsnCySlyr 44
 Db 76 AAAGCTCATGTCGCGCATCTGCTGCTGCTTAATGCATGAAACGGTAATGCATAATGCTAC 135
 QY 45 Pro 45
 Db 136 CCG 138
 RESULT 5
 ID AAF27525 standard; DNA; 180 BP.
 XX
 AC AAF27525;
 XX
 DT 28-MAR-2001 (first entry)
 DT
 DE Scorpion kallitoxin 2 precursor DNA #2.
 XX
 DE Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 XX
 KW Hottentotta judaica.
 KW
 PN WO200078958-A2.
 PN
 PD 28-DEC-2000.
 PD
 PF 21-JUN-2000; 2000WO-US017049.
 PF
 PR 22-JUN-1999; 99US-0140227P.
 PR
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 PI Herrmann R, Lee J, Wong JF;
 PI
 DR WPI; 2001-071394/08.
 DR
 XX

PT New polynucleotides encoding scorpion venom potassium-channel agonist
PT proteins for production e.g. of insect-tolerant transgenic plants for
PT controlling insect pest damage and parasitic worm infections.
XX
PS Claim 1; Page 45; 50pp; English.
XX
CC The present invention relates to scorpion toxins. The invention may be
CC used for the creation of transgenic plants which express K-channel
CC modifiers, useful as a means for controlling insect pests by producing
CC insect-tolerant plants. In the prevention and/or treatment of insect pest
CC damage and parasitic worm infections in animals and humans, the invention
CC may also find use in creating specific new pesticides and antihelmintic
CC drugs that are also non-toxic to humans, pets and livestock
XX
SQ Sequence 180 BP; 59 A; 27 C; 36 G; 58 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.00742 Length: 180
Score: 87.50 Matches: 18
Percent Similarity: 46.67% Conservative: 3
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 32.89% Indels: 1
Gaps: 1
DB:
US-10-614-934-14 (1-45) x AAF27525 (1-180)
Qy 1 MetMetIlePheCysGlnGlyAlaIleValSerIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 46 ATGACCATATGTTATTAATGCGCAATGAAACAAATGGAATGT--ACAGGTGGCTCA 102
Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaIleCysIleAsnIleThr 40
Db 103 TGTGCTTCACATGTAAAGAGATATAGAGTAGCTGACGAGAAATGATTAATGGAAGA 162
Qy 41 CysAsnCysTyrPro 45
Db 163 TGTGTCTGTATCCG 177
RESULT 6
AAQ84344
ID AAQ84344 standard; cDNA; 127 BP.
XX
AC AAQ84344;
XX
DT 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
XX
DE Constructed gene encoding scorpion margatoxin (MgTX).
XX
KM Scorpion venom; Centruroides margaritatus; margatoxin; MgTX;
KM synthetic gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..117
FT /*tag= a
XX
PN WO9503065-A1.
XX
PD 02-FEB-1995.
XX
PF 19-JUL-1994; 94WO-US008063.
XX
PR 22-JUL-1993; 93US-00096942.
XX
PA (MERI) MERCK & CO INC.
XX
PI Garcia ML, Koo GC, Leonard RJ, Lin C, Slaughter RS, Stevens SP;
PI Williamson JM;
XX
XX WPI; 1995-075021/10.
XX
DR P-PSDB; AAR66876.

XX
PT New purified scorpion venom peptide, Margatoxin - useful as a potent and
PT selective inhibitor of a voltage-dependent potassium channel as an
PT immunosuppressant.
XX
PS Claim 13; Page 31; 42pp; English.
XX
CC Margatoxin (MgTX) is purified to homogeneity from venom of the scorpion
CC C. margaritatus. The gene encoding MgTX is constructed and this gene is
CC expressed in E. coli to produce recombinant MgTX. MgTX is an inhibitor of
CC a voltage-dependent K+ channel present in human lymphocytes. It is useful
CC as an immunosuppressant. MgTX is useful as a selective probe for Kv1.3,
CC and may be employed in a screen for other Kv1.3 inhibitors exhibiting
CC immunosuppressant activity. MgTX inhibits interleukin 2 prodn. in human T
CC -lymphocytes (Lin et al., J. Exp. Med. 177, 637, 1993). (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 127 BP; 35 A; 37 C; 28 G; 27 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.00648 Length: 127
Score: 86.50 Matches: 15
Percent Similarity: 58.33% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 14
Query Match: 32.52% Indels: 1
Gaps: 1
DB:
US-10-614-934-14 (1-45) x AAQ84344 (1-127)
Qy 11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
Db 7 ATCAACGTTAAATGACCTCTCCGAAACAGTGCCTGCCGCCGCAAGCTCAGTTGGT 66
Qy 31 ThrArgAla--AlaIleCysIleAsnIleThrCysAsnCysTyrPro 45
Db 67 CAGTCTGTGCTGTATGATGATGACGTAATGCAAAATGCTACCCG 114
RESULT 7
AAF27532
ID AAF27532 standard; DNA; 174 BP.
XX
AC AAF27532;
XX
DT 28-MAR-2001 (first entry)
DT
XX
DE Scorpion Bmx1 DNA.
XX
KM Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
KM Hottentotia judaica.
XX
OS
XX
PN WO200078958-A2.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-US017049.
XX
PR 22-JUN-1999; 99US-0140227P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Herrmann R, Lee J, Wong JF;
XX
XX WPI; 2001-071394/08.
XX
XX
PT New polynucleotides encoding scorpion venom potassium-channel agonist
PT proteins for production e.g. of insect-tolerant transgenic plants for
PT controlling insect pest damage and parasitic worm infections.
XX
PS Claim 1; Page 48; 50pp; English.
XX
CC The present invention relates to scorpion toxins. The invention may be
CC used for the creation of transgenic plants which express K-channel

CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock

XX Sequence 174 BP, 51 A, 25 C, 37 G, 59 T, 0 U, 2 Other;

Alignment Scores:

Pred. No.:	0.00966	Length:	174
Score:	86.50	Matches:	17
Percent Similarity:	52.27%	Conservative:	6
Best Local Similarity:	38.64%	Mismatches:	20
Query Match:	32.52%	Indels:	1
DB:	4	Gaps:	1

US-10-614-934-14 (1-45) x AAF27532 (1-174)

QY 1 MetMetCIIePheCysGlnGlyGlnLysLysIleAsnTYrArgCysAsnAsnSerGlyGlu 20
 Db 40 ATAATGATTTCACCCGAACTCAG---TTTATAGACGTGAATGCATCACTAAGGAA 96

QY 21 CysIleProHisCysIleArgIleTYrAsnThrArgAlaIleLysCysIleAsnLysThr 40
 Db 97 TGTGGCCCTATTGTGAAGAAAGATTGTGTGCCAGAGAAAGTGATTAATTAAGCA 156

QY 41 CysAsnCysTYr 44
 Db 157 TGCCGTTCTTAT 168

RESULT 8

ABQ97088 ID ABQ97088 standard; cDNA; 231 BP.

XX AC ABQ97088;

XX DT 30-OCT-2002 (first entry)

XX DE Mouse ES cell related cDNA SEQ ID NO 356.

XX KM Mouse, ES cell; gene trapped sequence; GTS; gene expression;
 XX development disorder; cell differentiation disorder; gene; ss.

XX OS Mus sp.

XX PN US2002081668-A1.

XX PD 27-JUN-2002.

XX PF 30-NOV-2000; 2000US-00728446.

XX PR 20-NOV-1998; 98US-0109302P.

XX PR 01-DEC-1999; 99US-0168270P.

XX PA (FRIE// FRIEDRICH G.
 XX (ZAMB// ZAMBROWICZ B.
 XX (SAND// SANDS A T.

XX PI Friedrich G, Zambrowicz B, Sands AT;

XX DR WPI; 2002-626541/67.

XX Novel murine polynucleotides that individually identify novel genes into

PT which a retroviral gene trap vector has been integrated, useful in

PT genomic analysis and in discovery, development of therapeutic and

XX diagnostic agents.

PS Claim 2; SEQ ID NO 356; 29pp + Sequence Listing; English.

CC The invention relates to isolated murine polynucleotides (I) comprising a

CC contiguous stretch of at least about 60 nucleotides of a sequence

CC (ABQ96733-ABQ98191) chosen from 1461 OMNIBANK gene trapped sequences

CC (GTSs). The novel genes can be used in a process to identify novel

CC polynucleotide sequences by comparing them to the novel gene sequences.
 CC The novel genes and cells are useful in functional genomic analysis and
 CC in the discovery and development of new therapeutic and diagnostic agents
 CC and methods. (I) is useful for identifying the coding regions of the
 CC murine genome, to isolate cDNAs, genomic clones or full-length
 CC genes/polynucleotides or homologues, heterologues, paralogues or
 CC orthologues that are capable of hybridizing to one or more of the GTSs
 CC under stringent conditions. (I) can be incorporated into a phage display
 CC system that can be used to screen for proteins or other ligands, that are
 CC capable of binding an amino acid sequence encoded by an oligonucleotide
 CC or polynucleotide sequence in at least one of the GTS sequences. (I) is
 CC useful in arrays, such as gene chips, to identify and characterize
 CC temporal and tissue specific gene expression, to identify the gene of
 CC interest from many sources and for genetic manipulations such as
 CC antisense inhibition and gene targeting. Decreasing the level of
 CC expression of (I) and/or down regulating the activity of peptides or
 CC proteins encoded by (I) is useful for treating development and cell
 CC differentiation disorders. Note: the sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20020081668

XX Sequence 231 BP, 73 A, 47 C, 34 G, 77 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	0.119	Length:	231
Score:	79.50 <td>Matches:</td> <td>16 </td>	Matches:	16
Percent Similarity:	47.73% <td>Conservative:</td> <td>5 </td>	Conservative:	5
Best Local Similarity:	36.36% <td>Mismatches:</td> <td>20 </td>	Mismatches:	20
Query Match:	29.89% <td>Indels:</td> <td>3 </td>	Indels:	3
DB:	6 <td>Gaps:</td> <td>1 </td>	Gaps:	1

US-10-614-934-14 (1-45) x ABQ97088 (1-231)

QY 4 PheCysGlnGlyGlnLysLysIleAsnTYrArgCysAsnAsnSer-----GlyGlu 20
 Db 84 TTTCTCTCCAGACGAAAGCCCTTCTTGAAATTAATCATCAAAAAATTTTGGCCTC 143

QY 21 CysIleProHisCysIleArgIleTYrAsnThrArgAlaIleLysCysIleAsnLysThr 40
 Db 144 TGTTCCTCCATTTTGTGTGGAGATATATCCATCTTCTATTAATGGCAACTAGTAAT 203

QY 41 CysAsnCysTYr 44
 Db 204 TGTAAATGCTTT 215

RESULT 9

AAA48437 ID AAA48437 standard; cDNA; 180 BP.

XX AC AAA48437;

XX DT 15-SEP-2000 (first entry)

XX DE Scorpion potassium channel agonist Charybdotoxin 2 cDNA.

XX KM Scorpion; charybdotoxin 2; potassium channel agonist; insecticidal;
 XX insect-tolerant transgenic plant; ss.

XX OS Leturus quinquestratus.

XX PN MO200032777-A2.

XX PD 08-JUN-2000.

XX PF 01-DEC-1999; 99WO-US028351.

XX PR 02-DEC-1998; 98US-0110590P.

XX Key Location/Qualifiers

FT CDS 1..180

FT /*tag= a

FT /product= "Charybdotoxin 2"

```

XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Herrman R, Wong JF, Lu AL, Presnall JK, Lee J;
XX
XX WPI; 2000-422976/36.
XX P-PSDB; AAY99580.
XX
XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
XX channel agonist, useful for creating transgenic plants that are more
XX insect-tolerant.
XX
XX Claim 2; Page 42; 44pp; English.
XX
XX The present sequence encodes the scorpion potassium channel agonist
XX Charybdotoxin 2. The toxin forms a compact structure kept rigid by three
XX disulphide bonds. Potassium channels modulate a number of cellular events
XX such as muscle contraction, neuro-endocrine secretion, frequency and
XX duration of action potentials, electrolyte homeostasis and resting and
XX membrane potential. The agonist has a high affinity for the channel and
XX may therefore act by producing an irreversible blockade of the channel.
XX The nucleotide sequence was isolated from clone 1st.pK0018.e11 of a cDNA
XX library representing mRNAs from Leiurus scorpion telson tissues. The toxin
XX is insecticidal and the cDNA sequence can therefore be used to create
XX transgenic plants that express the toxin as a means of insect pest
XX control. The amino acid sequence of the present toxin shows homology to
XX the sequence of charybdotoxin 2 from Leiurus quinquestriatus (AAY99588)
XX
XX Sequence 180 BP; 57 A; 29 C; 33 G; 61 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.138 Length: 180
XX Score: 78.00 Matches: 13
XX Percent Similarity: 56.67% Conservative: 4
XX Best Local Similarity: 43.33% Mismatches: 13
XX Query Match: 29.32% Indels: 0
XX Gaps: 0
XX
XX US-10-614-934-14 (1-45) x AAA48437 (1-180)
XX
XX QY 15 CysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThrArgAlaAla 34
XX Db 85 TGCAGTGCATCTGCATCATGTTGGTGTGCTCAAACTGTATAAACACCTCAATGCA 144
XX
XX QY 35 LysCysIleAsnLysThrCysAsnCysTyr 44
XX Db 145 AAGGTATGAATATATAATGCCGCTGTAT 174
XX
XX RESULT 10
XX AAA48435
XX ID AAA48435 standard; cDNA; 150 BP.
XX
XX AC AAA48435;
XX
XX DT 15-SEP-2000 (first entry)
XX
XX DE Scorpion potassium channel agonist Charybdotoxin cDNA.
XX
XX KM Scorpion; charybdotoxin; potassium channel agonist; insecticidal;
XX insect-tolerant transgenic plant; ss.
XX
XX OS Leiurus quinquestriatus.
XX
XX Key Location/Qualifiers
XX CDS 1..150
XX FT /*tag= a
XX FT /partial
XX FT /product= "Charybdotoxin"
XX
XX WO200032777-A2.
XX
XX 08-JUN-2000.
XX

```

```

PF 01-DEC-1999; 99WO-US028351.
XX
XX 02-DEC-1998; 98US-0110590P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Herrman R, Wong JF, Lu AL, Presnall JK, Lee J;
XX
XX WPI; 2000-422976/36.
XX P-PSDB; AAY99578.
XX
XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
XX channel agonist, useful for creating transgenic plants that are more
XX insect-tolerant.
XX
XX Claim 2; Page 41; 44pp; English.
XX
XX The present sequence encodes the scorpion potassium channel agonist
XX Charybdotoxin. The toxin forms a compact structure kept rigid by three
XX disulphide bonds. Potassium channels modulate a number of cellular events
XX such as muscle contraction, neuro-endocrine secretion, frequency and
XX duration of action potentials, electrolyte homeostasis and resting and
XX membrane potential. The agonist has a high affinity for the channel and
XX may therefore act by producing an irreversible blockade of the channel.
XX The nucleotide sequence was isolated from clone 1st.pK0011.d2 of a cDNA
XX library representing mRNAs from Leiurus scorpion telson tissues. The toxin
XX is insecticidal and the cDNA sequence can therefore be used to create
XX transgenic plants that express the toxin as a means of insect pest
XX control. The amino acid sequence of the present toxin shows homology to
XX the sequence of charybdotoxin from Leiurus quinquestriatus (AAY99586)
XX
XX Sequence 150 BP; 43 A; 23 C; 37 G; 47 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.148 Length: 150
XX Score: 77.00 Matches: 13
XX Percent Similarity: 50.00% Conservative: 2
XX Best Local Similarity: 43.33% Mismatches: 15
XX Query Match: 28.95% Indels: 0
XX Gaps: 0
XX
XX US-10-614-934-14 (1-45) x AAA48435 (1-150)
XX
XX QY 15 CysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThrArgAlaAla 34
XX Db 58 TGTACTACATCTAAAGATGTTGGTCGTTGAGACATGTATTAAGACCAAGAGGA 117
XX
XX QY 35 LysCysIleAsnLysThrCysAsnCysTyr 44
XX Db 118 AAGTGCATGAATTTGAAATGCCGCTGTAT 147
XX
XX RESULT 11
XX AAF27530
XX ID AAF27530 standard; DNA; 176 BP.
XX
XX AC AAF27530;
XX
XX DT 28-MAR-2001 (first entry)
XX
XX DE Scorpion potassium channel blocking toxin 15-1 DNA.
XX
XX KM Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
XX
XX OS Hottentotta judaica.
XX
XX Key Location/Qualifiers
XX CDS 1..150
XX FT /*tag= a
XX FT /partial
XX FT /product= "Charybdotoxin"
XX
XX WO200078958-A2.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-US017049.
XX
XX 22-JUN-1999; 99US-0140227P.
XX

```

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 XX WPI, 2001-071394/08.
 DR
 XX New polynucleotides encoding scorpion venom potassium-channel agonist
 PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 PS Claim 1, Page 47, 50pp; English.
 XX
 CC The present invention relates to scorpion toxins. The invention may be
 CC used for the creation of transgenic plants which express K-channel
 CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock
 XX
 SQ Sequence 176 BP; 51 A; 24 C; 44 G; 57 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.336 Length: 176
 Score: 75.00 Matches: 13
 Percent Similarity: 52.94% Conservative: 5
 Best Local Similarity: 38.24% Mismatches: 16
 Query Match: 28.20% Indels: 0
 DB: 4 Gaps: 0
 US-10-614-934-14 (1-45) x AAF27530 (1-176)
 QY 11 IleaenTYrRGcYsAenAsnserGlyuCYsileProhiscYsileArglyeTyraSn 30
 Db 73 ATAGACGTAAAGTAGTGGCTCTGCTGATGTTGGAGACTTGAGAAAAGTAACAGGA 132
 QY 31 ThrArgAlaAlaAlaYsCYsileAsnlySThCYsAsnCYsTYr 44
 Db 133 TCAGGACAAAGAAAGTGCACAAATACCAATCTCGTTGTAT 174
 RESULT 12
 AAA48430
 ID AAA48430 standard; cDNA; 177 BP.
 XX
 AC AAA48430;
 XX
 DT 15-SEP-2000 (first entry)
 XX
 DE Scorpion potassium channel blocking toxin 15-1 cDNA.
 XX
 KW Scorpion; potassium channel agonist; insecticidal;
 KW insect-tolerant transgenic plant; potassium channel blocking toxin 15-1;
 XX
 KM 88.
 XX
 OS Leiurus quinquestriatus.
 XX
 OS
 FT Key Location/Qualifiers
 FT CDS 1..177
 FT /tag= a
 FT /product= "Potassium channel blocking toxin 15-1"
 XX
 PN WO200032777-A2.
 XX
 PD 08-JUN-2000.
 XX
 PE 01-DEC-1999; 99WO-US028351.
 XX
 PR 02-DEC-1998; 98US-0110590P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Wong JF, Lu AL, Preenail JK, Lee J;
 XX

DR WPI, 2000-422976/36.
 DR P-PSDB; AAY99573.
 XX
 XX New nucleic acid fragment encoding a scorpion toxin that is a potassium
 PT channel agonist, useful for creating transgenic plants that are more
 PT insect-tolerant.
 XX
 PS Claim 2, Page 39, 44pp; English.
 XX
 CC The present sequence encodes the scorpion potassium channel blocking
 CC toxin 15-1. The toxin is a potassium channel agonist which forms a
 CC compact structure kept rigid by three disulphide bonds. Potassium
 CC channels modulate a number of cellular events such as muscle contraction,
 CC neuro-endocrine secretion, frequency and duration of action potentials,
 CC electrolyte homeostasis and resting membrane potential. The agonist has a
 CC high affinity for the channel and may therefore act by producing an
 CC irreversible blockade of the channel. The nucleotide sequence was
 CC isolated from clone 18c.pK0005.c5 of a cDNA library representing mRNAs
 CC from Leiurus scorpion telson tissues. The toxin is insecticidal and the
 CC cDNA sequence can therefore be used to create transgenic plants that
 CC express the toxin as a means of insect pest control. The amino acid
 CC sequence of the present toxin shows homology to the sequence of potassium
 CC channel blocking toxin 15-1 from Leiurus quinquestriatus (AAY99581)
 XX
 SQ Sequence 177 BP; 56 A; 25 C; 39 G; 57 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.626 Length: 177
 Score: 73.00 Matches: 14
 Percent Similarity: 45.00% Conservative: 4
 Best Local Similarity: 35.00% Mismatches: 22
 Query Match: 27.44% Indels: 0
 DB: 3 Gaps: 0
 US-10-614-934-14 (1-45) x AAA48430 (1-177)
 QY 5 CysGinglyGlnlySlySileAsnTYrRGcYsAsnAsnserGlyuCYsileProhisc 24
 Db 55 TGTAGTGAAGCTGGAGCTCATAGAGTATGTTTGCATCTCGGAATGTTGGAGACT 114
 QY 25 CysileArglyeTYrAsnThrArgAlaAlaYsCYsileAsnlySThCYsAsnCYsTYr 44
 Db 115 TGCAGAAAAGTAAACAGATCGGACCAAGAAAATGCCAGAAATATCATGTCGCTGAT 174
 RESULT 13
 AAF27531
 ID AAF27531 standard; DNA; 177 BP.
 XX
 AC AAF27531;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Scorpion potassium channel blocking toxin 15-1 DNA #2.
 XX
 KW Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 XX
 KM Hottentotta judaica.
 XX
 OS
 FT Key Location/Qualifiers
 FT CDS WO200078958-A2.
 FT /tag= a
 FT /product= "Potassium channel blocking toxin 15-1"
 XX
 PD 28-DEC-2000.
 XX
 PE 21-JUN-2000; 2000WO-US017049.
 XX
 PR 22-JUN-1999; 99US-0140227P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 XX WPI, 2001-071394/08.
 DR New polynucleotides encoding scorpion venom potassium-channel agonist
 PT

PT proteins for production e.g. of insect-tolerant transgenic plants for
PT controlling insect pest damage and parasitic worm infections.
XX
PS Claim 1; Page 47; 50pp; English.
XX
CC The present invention relates to scorpion toxins. The invention may be
CC used for the creation of transgenic plants which express K-channel
CC modifiers, useful as a means for controlling insect pests by producing
CC insect-tolerant plants. In the prevention and/or treatment of insect pest
CC damage and parasitic worm infections in animals and humans, the invention
CC may also find use in creating specific new pesticides and antihelmintic
CC drugs that are also non-toxic to humans, pets and livestock
XX
SQ Sequence 177 BP, 61 A, 22 C, 31 G, 63 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 1.16 Length: 177
Score: 71.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 26.69% Indels: 0
DB: Gaps: 0
US-10-614-934-14 (1-45) x AAF27531 (1-177)

QY 11 TLeAsnTyArGcYsAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyAsn 30
Db 73 ATAGACGTAATAAGTTTGCATCTCAAGAAATGTTGATTCGTTAAAGTAACAGCA 132

QY 31 ThrArgAlaAlaIleCysIleAsnIleThrCysAsnCysTyR 44
Db 133 CGGTTTCAAGAAATGCGCAGATTAACATATGCGTGTAT 174

RESULT 14
ADRI3786
ID ADRI3786 standard; DNA; 435 BP.
XX
AC ADRI3786;
XX
DT 23-SEP-2004 (first entry)
XX
DE Chinese scorpion marten toxin peptide coding sequence.
XX
KW Chinese scorpion; marten toxin; potassium channel blocker; ds; gene.
XX
OS Mesobuthus marteni.
XX
PN CN1344745-A.
XX
PD 17-APR-2002.
XX
PF 12-OCT-2001; 2001CN-00131909.
XX
PR 12-OCT-2001; 2001CN-00131909.
XX
PA (UIYY) JI Y.
XX
PI Ji Y, Li Y, Ye J;
XX
DR WPI; 2002-509500/55
XX
P-PSDB; ADRI3780, ADRI3781, ADRI3790.
XX
PT Marten toxin as one great-conductance calcium-activating potassium channel
XX blocker and its preparation.
XX
PS Disclosure; SEQ ID NO 7; 30pp; Chinese.
XX
CC The invention comprises the amino acid and coding sequence of a Chinese
CC scorpion marten toxin peptide. The marten toxin peptide of the invention is
CC useful as a potassium channel blocker. The present DNA sequence encodes
CC the Chinese scorpion marten toxin peptide of the invention.
XX
SQ Sequence 435 BP, 148 A, 51 C, 67 G, 169 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 4.93 Length: 435
Score: 70.00 Matches: 12
Percent Similarity: 50.00% Conservative: 5
Best Local Similarity: 35.29% Mismatches: 17
Query Match: 26.32% Indels: 0
DB: Gaps: 0
US-10-614-934-14 (1-45) x ADRI3786 (1-435)

QY 11 TLeAsnTyArGcYsAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyAsn 30
Db 298 ATAGACGTAATAAGTTTGCATCTCAAGAAATGTTGATTCGTTAAAGTAACAGCA 357

QY 31 ThrArgAlaAlaIleCysIleAsnIleThrCysAsnCysTyR 44
Db 358 TCGGACACAGAAAGTCCAGAAATTAATCATATGTCGATC 399

RESULT 15
ABN60476/C
ID ABN60476 standard; cDNA; 598 BP.
XX
AC ABN60476;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human cancer related polynucleotide SEQ ID NO 443.
XX
KW Human; cytotoxic; gene expression; gene mapping; tissue profiling;
KW gene therapy; cancer; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200214500-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US025840.
XX
PR 16-AUG-2000; 2000US-0226326P.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F,
PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
XX
DR WPI; 2002-241905/29.
XX
XX
PT New nucleic acid for producing a polypeptide, detecting differentially
PT expressed genes correlated with a cancerous state of a mammalian cell,
PT and inhibiting tumor growth.
XX
PS Claim 1; SEQ ID NO 443; 883pp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
CC with cytotoxic activity. The polynucleotide is used to produce a
CC polypeptide, to detect differentially expressed genes correlated with a
CC cancerous state of a mammalian cell and to inhibit tumor growth. The
CC polynucleotide is used as a probe in mapping and tissue profiling. The
CC encoded polypeptide and antibodies to the polypeptide can also be used
CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
CC gene therapy. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 598 BP, 232 A, 111 C, 134 G, 121 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 7.38 Length: 598
Score: 70.00 Matches: 17
Percent Similarity: 50.98% Conservative: 9

Best Local Similarity: 33.33% Mismatches: 13
Query Match: 26.32% Indels: 12
DB: 6 Gaps: 4

US-10-614-934-14 (1-45) x ABN60476 (1-598)

```
OY      5  CysGlnGlyGlnLysLysIle---AsnTyrArgCysAsnAsnSerGlyGluCysIlePro 23
          |||::|||
          168 TGTCTGGGCGCTTCAAGAGCTGGGATGTACAGGTGTAGAGCCCGTG-----TGTCTGGAGC 115
Db
OY      24 HisCysIleArgIleTyrAsnThrArgAlaAlaLysCys-----IleAsn 38
          |||::|||
          114 TACTGCACGCTTTTCTACAGCTACTAGTTTAAATGCAACCACTCATGTAAATATCA 55
OY      39 LysThrCys-----AsnCysTyrPro 45
          |||::|||
          54 GAGACTTGCAAAAGTCTAATTCTGTCTTCTCT 22
Db
```

Search completed: August 19, 2005, 05:11:53
Job time : 436 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 04:24:18 ; Search time 3109 seconds

(without alignments)
550.946 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MMIFCQCKINRYCNSNGE.....IRYNTBAKCNKTCNCP 45

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool_p/US10614934/runat_17082005_181357_22105/app_query.fasta_1.199
-DB=EST -QFWT=fastap -SUFFIX=rcs -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blissum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10614934@cgn2.1 1.5180 @runat_17082005_181357_22105 -NCPu=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEX=7

Database : EST:*

1: gb_esc1:*\n2: gb_esc2:*\n3: gb_hic:*\n4: gb_esc3:*\n5: gb_esc4:*\n6: gb_esc5:*\n7: gb_esc6:*\n8: gb_ges1:*\n9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	79.5	29.9	526	B0033213	UI-1-CFO-B0033213 UI-1-CFO-
C 2	79.5	29.9	766	AGS06152	AGS06152 Mus muscu
C 3	79.5	29.9	840	CR177814	CR177814 Forward s
C 4	79.5	29.9	850	BX977811	BX977811 Forward s
C 5	79.5	29.9	865	CR245225	CR245225 Forward s
C 6	79.5	29.9	874	CR257546	CR257546 Forward s
C 7	79.5	29.9	769	CK173729	CK173729 EST763049
C 8	73	27.4	794	AGS86472	AGS86472 Mus muscu
C 9	72	27.1	187	CV087408	CV087408 est_c_vir

C 10	72	27.1	345	7	CV087152	est_c_vir
C 11	72	27.1	345	7	CV087280	est_c_vir
C 12	72	27.1	345	7	CV087696	est_c_vir
C 13	72	27.1	345	7	CV087806	est_c_vir
C 14	72	27.1	623	6	CB018045	pgn1c.pk0
C 15	72	27.1	967	4	BG420272	602448285
C 16	71.5	26.9	605	6	CB280757	
C 17	71.5	26.9	870	9	CC697521	OSVETB5TC
C 18	71.5	26.9	932	8	B2966071	PUDFQ58TD
C 19	71.5	26.9	932	8	CC389822	PUMMT74TD
C 20	71.5	26.9	964	9	CC697530	OGVETB5TM
C 21	70.5	26.5	335	4	BM282738	k139h06.y
C 22	70	26.3	333	2	BB254078	BB254078
C 23	70	26.3	562	9	BX238124	Danilo rer
C 24	69.5	26.1	269	2	BB438608	BB438608
C 25	69.5	26.1	742	9	AG023370	Oryza sat
C 26	69.5	26.1	793	8	AZ135495	OSJNB011
C 27	69.5	26.1	810	7	CK129706	AGNRCOURT
C 28	69	25.9	646	5	B0345684	603524173
C 29	68.5	25.8	604	1	AA156020	z048b07.s
C 30	68.5	25.8	711	9	AG351862	Mus muscu
C 31	68.5	25.8	844	8	AZ540533	
C 32	68.5	25.8	861	8	AZ544428	ENTES79TR
C 33	68.5	25.8	882	8	AZ668455	ENTMC78TR
C 34	68.5	25.8	899	8	AZ670025	ENTMB20TR
C 35	68.5	25.8	900	8	BZ697287	PUNIB94TD
C 36	68.5	25.8	902	8	AZ540783	ENTDG03TR
C 37	68.5	25.8	916	8	BH135823	ENTQO20TR
C 38	68.5	25.8	940	8	BZ699102	PUMM294TD
C 39	68.5	25.8	960	8	BZ700560	PUBNA94TD
C 40	68.5	25.8	1163	1	AV278106	CH261-64A
C 41	68	25.6	211	1	AV278106	AV278106
C 42	68	25.6	368	8	AQ139514	HS 3088.A
C 43	68	25.6	397	9	CR191328	Forward s
C 44	68	25.6	577	9	CE567579	tigt-gss-
C 45	68	25.6	690	5	B0324729	603489543

ALIGNMENTS

RESULT 1
B0033213/c
LOCUS
DEFINITION
UI-1-CFO-axp-g-12-0-UI-s1 NCI CGAP PITr1 Mus musculus cDNA clone
UI-1-CFO-axp-g-12-0-UI 3', mRNA sequence.

ACCESSION
B0033213
VERSION
B0033213.1
KEYWORDS
B0033213.1 GI:19768492
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 526)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rosent, Dr. Janet

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-22, >AT rich#low complexity 33-257,
>MER67B#LTR/MER4-group (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1..526
location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 5.22 Length: 840
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x CR177814 (1-840)

QY 4 PheCysGInGlyAluLysIleAsnTyRarGysAsnAsnSer-----GlyGlu 20
 DB 772 TTTCCTCCAGACAGAAAGCCCTTCCTTGAATGTAAATCATCAAAAAATTTGGCGTC 713

QY 21 CysIleProHisCysIleArgIleTyRAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 712 TGTTCCTCCATTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCCACTAGTAAT 653

QY 41 CysAsnCySTyr 44
 DB 652 TGTATTTGCTTT 641

RESULT 4

BX977811/c

LOCUS BX977811 850 bp DNA linear GSS 05-JUL-2004
 DEFINITION Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN33h07, genomic survey sequence.

ACCESSION BX977811 GI:49709234
 VERSION BX977811.1
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES

source 1..850
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN33h07"
 /clone_lib="MHPN"

ORIGIN

Alignment Scores:

Pred. No.: 5.3 Length: 850
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x BX977811 (1-850)

QY 4 PheCysGInGlyAluLysIleAsnTyRarGysAsnAsnSer-----GlyGlu 20
 DB 770 TTTCCTCCAGACAGAAAGCCCTTCCTTGAATGTAAATCATCAAAAAATTTGGCGTC 711

QY 21 CysIleProHisCysIleArgIleTyRAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 710 TGTTCCTCCATTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCCACTAGTAAT 651

QY 41 CysAsnCySTyr 44
 DB 650 TGTATTTGCTTT 639

RESULT 5

CR245225/c

LOCUS CR245225 865 bp DNA linear GSS 06-JUL-2004
 DEFINITION Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN98f06, genomic survey sequence.

ACCESSION CR245225 GI:50024079
 VERSION CR245225.1
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES

source 1..865
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN98f06"
 /clone_lib="MHPN"

ORIGIN

Alignment Scores:

Pred. No.: 5.41 Length: 865
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

US-10-614-934-14 (1-45) x CR245225 (1-865)

QY 4 PheCysGInGlyAluLysIleAsnTyRarGysAsnAsnSer-----GlyGlu 20
 DB 781 TTTCCTCCAGACAGAAAGCCCTTCCTTGAATGTAAATCATCAAAAAATTTGGCGTC 722

QY 21 CysIleProHisCysIleArgIleTyRAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 DB 721 TGTTCCTCCATTTGTGTGGGAAGATATATATCCCATCTTCTATATTTGCCCACTAGTAAT 662

QY 41 CysAsnCySTyr 44
 DB 661 TGTATTTGCTTT 650

RESULT 6

CR257546/c

LOCUS CR257546 874 bp DNA linear GSS 06-JUL-2004
 DEFINITION Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN248m09, genomic survey sequence.

ACCESSION CR257546 GI:50036399
 VERSION CR257546.1
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES

source 1..874
 /organism="Mus musculus"

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	
LOCUS CV087408/c	187 bp mRNA linear EST 26-AUG-2004	est_c_virginica416	Cv Hemo 4hr Immune Forward SSH Crassostrea virginica cDNA, mRNA sequence.	CV087408	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 187)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@musc.edu.	Location/Qualifiers 1..187 /organism="Crassostrea virginica" /mol_type="mRNA" /db_xref="taxon:6565" /cell_type="Hemocyte" /clone_lib="Cv Hemo 4hr Immune Forward SSH" /note="Vector: PCR2.1; Site_1: none; Site_2: none"	
Db	604	TGTCACCTTAC	593										
Qy	21	CysAaenSerglyu	44										
Db	661	TTCATTTCCCACTGATTT	---	GTATTTAAAC	CTGTACTTAACGACAGTGTCTGTAA	GACA	605						
Qy	41	CysAaenSerglyu	44										
Db	604	TGTCACCTTAC	593										
RESULT 9	CV087408/c	187 bp mRNA linear EST 26-AUG-2004	est_c_virginica416	Cv Hemo 4hr Immune Forward SSH Crassostrea virginica cDNA, mRNA sequence.	CV087408	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 187)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@musc.edu.	Location/Qualifiers 1..187 /organism="Crassostrea virginica" /mol_type="mRNA" /db_xref="taxon:6565" /cell_type="Hemocyte" /clone_lib="Cv Hemo 4hr Immune Forward SSH" /note="Vector: PCR2.1; Site_1: none; Site_2: none"
LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	
LOCUS CV087152/c	345 bp mRNA linear EST 26-AUG-2004	est_c_virginica186	Cv Hemo Cadmium Rev SSH Crassostrea virginica cDNA, mRNA sequence.	CV087152	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 345)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@musc.edu.	Location/Qualifiers 1..345 /organism="Crassostrea virginica" /mol_type="mRNA" /db_xref="taxon:6565" /cell_type="Hemocyte" /clone_lib="Cv Hemo Cadmium Rev SSH Crassostrea virginica" /note="Vector: PCR2.1; Site_1: none; Site_2: none"	
Db	115	TGCAACAACATACGATGTTGTTCCGCCCACTGC	-----	GACCCACATTTCTGA	68								
Qy	35	LybCysAaenSerglyu	43										
Db	67	ACTGTATTCACCAACCAATGACCACTGT	41										
RESULT 10	CV087152/c	345 bp mRNA linear EST 26-AUG-2004	est_c_virginica186	Cv Hemo Cadmium Rev SSH Crassostrea virginica cDNA, mRNA sequence.	CV087152	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 345)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@musc.edu.	Location/Qualifiers 1..345 /organism="Crassostrea virginica" /mol_type="mRNA" /db_xref="taxon:6565" /cell_type="Hemocyte" /clone_lib="Cv Hemo Cadmium Rev SSH Crassostrea virginica" /note="Vector: PCR2.1; Site_1: none; Site_2: none"
LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	
LOCUS CV087152/c	345 bp mRNA linear EST 26-AUG-2004	est_c_virginica186	Cv Hemo Cadmium Rev SSH Crassostrea virginica cDNA, mRNA sequence.	CV087152	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 345)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843 792 4850 Email: gross@musc.edu.	Location/Qualifiers 1..345 /organism="Crassostrea virginica" /mol_type="mRNA" /db_xref="taxon:6565" /cell_type="Hemocyte" /clone_lib="Cv Hemo Cadmium Rev SSH Crassostrea virginica" /note="Vector: PCR2.1; Site_1: none; Site_2: none"	
Db	115	TGCAACAACATACGATGTTGTTCCGCCCACTGC	-----	GACCCACATTTCTGA	68								
Qy	35	LybCysAaenSerglyu	43										
Db	67	ACTGTATTCACCAACCAATGACCACTGT	41										
RESULT 10	CV087152/c	345 bp mRNA linear EST 26-AUG-2004	est_c_virginica186	Cv Hemo Cadmium Rev SSH Crassostrea virginica cDNA, mRNA sequence.	CV087152	Crassostrea virginica (eastern oyster)	Crassostrea virginica	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreoida; Ostreidae; Crassostrea.	1 (bases 1 to 345)	Jenny, M.J., Watt, G.W., Gross, P.S., Almeida, J.S., Chen, Y., McKillen, D.J., Wu, S. and Chapman, R.W.	Crassostrea virginica EST library at marinesgenomics.org Unpublished (2004)	Contact: Gross PS Department of Biochemistry and Molecular Biology Medical University of South Carolina Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA Tel: 846 792 8503 Fax: 843	

```

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087280 (1-345)

QY 15 Cysaasnsersgylgucysileprohiscysilearglietyraanttharagalaala 34
Db 120 TGCACACACATGCTGATTGTCGCCACCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysileanlysthrCysaancys 43
Db 72 ACTTGATCAACACCAATGCCACTGT 46

RESULT 12
CV087696 345 bp mRNA linear EST 26-AUG-2004
LOCUS est_c_virginica017 Cv Hepato Cadmium Forward SSH Crassostrea
ACCESSION CV087696 GI:51567045
VERSION CV087696.1 GI:51567045
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 345)
AUTHORS Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
McKillen,D.J., Wu,S. and Chapman,R.W.
Crassostrea virginica EST Library at marinegenomics.org
JOURNAL Unpublished (2004)
COMMENT Contact: Gross PS
Department of Biochemistry and Molecular Biology
Medical University of South Carolina
Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
Tel: 846 792 8503
Fax: 843 792 4850
Email: grossp@musc.edu.
FEATURES
source
1..345
Location/Qualifiers
/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="hepatopancreas"
/clone_lib="Cv Hepato Cadmium Forward SSH"
/notes="Vector: pCR2.1; Site_1: none; Site_2: none"

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087696 (1-345)

QY 15 Cysaasnsersgylgucysileprohiscysilearglietyraanttharagalaala 34
Db 120 TGCACACACATGCTGATTGTCGCCACCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysileanlysthrCysaancys 43
Db 72 ACTTGATCAACACCAATGCCACTGT 46

RESULT 12
CV087696 345 bp mRNA linear EST 26-AUG-2004
LOCUS est_c_virginica017 Cv Hepato Cadmium Forward SSH Crassostrea
ACCESSION CV087696 GI:51567045
VERSION CV087696.1 GI:51567045
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 345)
AUTHORS Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
McKillen,D.J., Wu,S. and Chapman,R.W.
Crassostrea virginica EST Library at marinegenomics.org
JOURNAL Unpublished (2004)
COMMENT Contact: Gross PS
Department of Biochemistry and Molecular Biology
Medical University of South Carolina
Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
Tel: 846 792 8503
Fax: 843 792 4850
Email: grossp@musc.edu.
FEATURES
source
1..345
Location/Qualifiers
/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="hemocyte"
/clone_lib="Cv Hemo 4hr Immune Reverse SSH"
/notes="Vector: pCR2.1; Site_1: none; Site_2: none"

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087806 (1-345)

QY 15 Cysaasnsersgylgucysileprohiscysilearglietyraanttharagalaala 34
Db 120 TGCACACACATGCTGATTGTCGCCACCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysileanlysthrCysaancys 43
Db 72 ACTTGATCAACACCAATGCCACTGT 46

RESULT 14
CB018045 623 bp mRNA linear EST 10-JAN-2003
LOCUS pgnic.pk018.012 Chicken lymphoid cDNA library (pgnic) Gallus gallus
DEFINITION cDNA clone pgnic.pk018.012 5' similar to no significant hits
(plog(P) 4), mRNA sequence.
ACCESSION CB018045 GI:27592781
VERSION CB018045.1 GI:27592781
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 623)
AUTHORS Morgan,R.W. and Burnside,J.
TITLE Chicken ESTs from lymphoid tissue
JOURNAL Unpublished (2002)
COMMENT Contact: Robin W. Morgan
University of Delaware

```

```

RESULT 13
CV087806 345 bp mRNA linear EST 26-AUG-2004
LOCUS est_c_virginica546 Cv Hemo 4hr Immune Reverse SSH Crassostrea
DEFINITION virginica cDNA, mRNA sequence.
ACCESSION CV087806 GI:51567155
VERSION CV087806.1 GI:51567155
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 345)
AUTHORS Jenny,M.J., Marr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
McKillen,D.J., Wu,S. and Chapman,R.W.
Crassostrea virginica EST Library at marinegenomics.org
JOURNAL Unpublished (2004)
COMMENT Contact: Gross PS
Department of Biochemistry and Molecular Biology
Medical University of South Carolina
Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
Tel: 846 792 8503
Fax: 843 792 4850
Email: grossp@musc.edu.
FEATURES
source
1..345
Location/Qualifiers
/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="hemocyte"
/clone_lib="Cv Hemo 4hr Immune Reverse SSH"
/notes="Vector: pCR2.1; Site_1: none; Site_2: none"

ORIGIN
Alignment Scores:
Pred. No.: 17.4 Length: 345
Score: 72.00 Matches: 11
Percent Similarity: 55.17% Conservative: 5
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 27.07% Indels: 4
DB: 7 Gaps: 1

US-10-614-934-14 (1-45) x CV087806 (1-345)

QY 15 Cysaasnsersgylgucysileprohiscysilearglietyraanttharagalaala 34
Db 120 TGCACACACATGCTGATTGTCGCCACCATCTGC-----GACCCACATTCTGGA 73

QY 35 LysCysileanlysthrCysaancys 43
Db 72 ACTTGATCAACACCAATGCCACTGT 46

RESULT 14
CB018045 623 bp mRNA linear EST 10-JAN-2003
LOCUS pgnic.pk018.012 Chicken lymphoid cDNA library (pgnic) Gallus gallus
DEFINITION cDNA clone pgnic.pk018.012 5' similar to no significant hits
(plog(P) 4), mRNA sequence.
ACCESSION CB018045 GI:27592781
VERSION CB018045.1 GI:27592781
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 623)
AUTHORS Morgan,R.W. and Burnside,J.
TITLE Chicken ESTs from lymphoid tissue
JOURNAL Unpublished (2002)
COMMENT Contact: Robin W. Morgan
University of Delaware

```


Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1341
Fax: 302 831-2822
Email: morganeludel.edu, www.chickest.udel.edu.

FEATURES

SOURCE

Location/Qualifiers
1. 623

/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgnic.pk018.012"
/sex="Male and Female"
/tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli BMD10B"
/clone_lib="Chicken lymphoid cDNA library (pgnic)"
/note="Vector: pCMVSPORT 6"

ORIGIN

Alignment Scores:

Pred. No.: 35.9 Length: 623
Score: 72.00 Matches: 17
Percent Similarity: 46.81% Conservative: 5
Best Local Similarity: 36.17% Mismatches: 11
Query Match: 27.07% Indels: 14
DB: 6 Gaps: 3

US-10-614-934-14 (1-45) x CB018045 (1-623)

Qy 11 l l e a n t y r a r g c y a a n a n s e r g l y g l u ----- Cys 21

Db 223 A T T A A C A C T T A T A A T A G A G A G G T T C T C T A A A T C A G C A G C C C G G G T G C T T 282

Qy 22 l l e p r o h i s c y s i l e a r g i l e t y r a n t h r a r g a l a l a l a y s c y a i l e a n l y e t h r c y s 41

Db 283 A T G C T T C A C A G C A G A G A G T T A T A T ----- G C C G A A A A T G T T A T C T C A T T A T G T 336

Qy 42 A a n c y s ----- T y r p r o 45

Db 337 A A C T G T G A T G T G A T T A C C C A 357

RESULT 15

BG420272/c 967 bp mRNA linear EST 14-MAR-2001

LOCUS 602448285F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586972 5',
DEFINITION mRNA sequence.

ACCESSION BG420272

VERSION BG420272.1 GI:13326778

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 967)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgsrbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

http://image.llnl.gov

Plate: LNCM1316 row: 1 column: 21

High quality sequence start: 9

High quality sequence stop: 678.

Location/Qualifiers

1. 967

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4586972"

/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 14"
/note="Organ: kidney; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 61.6 Length: 967
Score: 72.00 Matches: 14
Percent Similarity: 61.29% Conservative: 5
Best Local Similarity: 45.16% Mismatches: 8
Query Match: 27.07% Indels: 4
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x BG420272 (1-967)

Qy 3 l l e p h e c y s g i n g l y g l n l y s l e a n t y r a r g c y a a n a n s e r g l y g l u c y s i l e 22

Db 780 A T T T T T G T A T G T G A A A T G A A C T T A T C A T G A G G T G C C A C A C T C T G T G A C ----- 727

Qy 23 P r o h i s c y s i l e a r g i l e t y r a n t h r a r g l a 33

Db 726 ----- T G T G T C G G T T T C A T A C A C A G G G C A 700

Search completed: August 19, 2005, 06:33:27
Job time : 3114 secs

This page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 10:20:42 ; Search time 131 Seconds

(without alignments)
562.080 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MMIFCQKIKINRNNGSE.....IRIYNTRAKINCNCYP 45

Scoring table:
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US1061934/rnat_19082005_112037_24047/app_query.fasta_1.199
-DB=Issued_Patents_NA -QEMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10614934 @CGN 1.1.105 @rnat_19082005_112037_24047 -NCPU=6 -ICPU=3
-NO MAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	100.0	138	4	US-09-857-401B-13
2	101	38.0	114	4	US-09-857-401B-9
3	92.5	34.8	186	4	US-10-044-359-3
4	91.5	34.4	154	1	US-08-096-942-5
5	91.5	34.4	154	1	PCR-US94-08063-5
6	87.5	33.9	180	4	US-10-044-359-5
7	86.5	33.5	120	1	US-08-096-942-2
8	86.5	33.5	174	4	US-10-044-359-19
9	78	23.3	180	4	US-09-857-401B-15
10	77	28.9	150	4	US-09-857-401B-11
11	75	28.2	176	4	US-10-044-359-15
12	73	27.4	177	4	US-09-857-401B-1

13	71	26.7	177	4	US-10-044-359-17
14	68.5	25.8	127	5	PCT-US94-08063-2
15	68.5	25.8	124700	4	US-09-949-016-11817
16	68.5	25.8	124701	4	US-09-949-016-15439
17	67.5	25.4	643	4	US-09-270-767-5432
18	67.5	25.4	643	4	US-09-270-767-20714
19	64	24.1	601	4	US-09-949-016-51773
20	64	24.1	146095	4	US-09-949-016-12872
21	64	24.1	146104	4	US-09-949-016-13239
22	63	23.7	891	4	US-09-810-886B-7
23	63	23.7	2940	3	US-08-688-431-28
24	63	23.7	2940	3	US-09-389-558-28
25	63	23.7	2940	3	US-09-181-827A-28
26	62	23.3	544	4	US-09-621-976-15220
27	62	23.3	636591	4	US-09-949-016-11808
28	62	23.3	636591	4	US-09-949-016-13388
29	61.5	23.1	817	4	US-09-270-767-12401
30	61.5	23.1	2964	2	US-08-286-819A-18
31	61.5	23.1	2964	3	US-08-980-357-18
32	61.5	23.1	3190	2	US-08-286-819A-30
33	61.5	23.1	3190	3	US-08-980-357-30
34	61.5	23.1	7577	3	US-08-961-537-46
35	61.5	23.1	10851	2	US-08-286-819A-16
36	61.5	23.1	10851	3	US-08-980-357-16
37	61	22.9	1167	4	US-09-489-039A-1018
38	60.5	22.7	640	4	US-08-956-171E-418
39	60.5	22.7	640	4	US-08-781-986A-418
40	60.5	22.7	2581	1	US-08-200-900A-1
41	60.5	22.7	2581	4	US-08-794-042-1
42	60.5	22.7	3576	5	PCT-US94-00616-1
43	60.5	22.7	3576	4	US-09-540-236-982
44	60	22.6	349	4	US-09-621-976-15221
45	60	22.6	1128	3	US-08-976-259-25

ALIGNMENTS:

US-09-857-401B-13
Sequence 13, Application US/09857401B
Patent No. 6593141
GENERAL INFORMATION:
APPLICANT: HERRMANN, RAFAEL
APPLICANT: WONG, JAMES F.
APPLICANT: LU, ALBERT L.
APPLICANT: PRESNALL, JAMES K.
APPLICANT: LEE, JIAN-MING
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1102
CURRENT APPLICATION NUMBER: US/09/857,401B
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/110,590
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 138
TYPE: DNA
ORGANISM: Leiurus quinquestriatus
US-09-857-401B-13

Alignment Scores:
Pred. No.: 3.58e-29
Score: 266.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-10-614-934-14 (1-45) x US-09-857-401B-13 (1-138)
QY 1 MetMetIlePheCysGlnGlyClnLysIleAsnTYRArgCysAsnAsnSerGlyGlu 20
|||||

```

Db      1  ATGATGATTTTCTGCGAAGCCGCAAGAAAAATATAATTAATGATGATATATAGCGGTGAG
QY      21  CyslleProHisCyslleArgilleTyraAsnThrArgAlaIalaIysCyslleAsnIysThr
Db      61  TGTATTCACATTCATCATCGAGATATATATTAACACGACGACGAAAGTGTATTAATAAACA
QY      41  CysAsnCysTyPro 45
Db      121 TGCATTTGTTATCA 135

RESULT 2
US-09-857-401B-9
; Sequence 9, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERMANN, RAPHAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Leiurus quinquestriatus
US-09-857-401B-9

Alignment Scores:
Pred. No.:      4,63e-06      Length:      114
Score:          101.00      Matches:      17
Percent Similarity: 58.82%      Conservative: 3
Best Local Similarity: 50.00%      Mismatches: 14
Query Match:      37.97%      Indels:      0
DB:               4          Gaps:      0

US-10-614-934-14 (1-45) x US-09-857-401B-9 (1-114)
QY      12  AsnTyraArgCysAsnAsnSerGlyIuCyslleProHisCyslleArgIleTyraAsnThr 31
Db      10  AATGTGCCGGGCAAGAAATTTCTGACATGTCGTCGATTAAGAAAGATTAATAT 69
QY      32  ArgAlaIalaIysCyslleAsnIysThrCysAsnCysTyPro 45
Db      70  AATAGCGAAGAGTGTGTTATGACAAATGATTTGTTATCCA 111

RESULT 3
US-10-044-359-3
; Sequence 3, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: HERTMAN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B11367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/539,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 186
; TYPE: DNA

```

```

; ORGANISM: Hottentotta judaica
US-10-044-359-3

Alignment Scores:
Pred. No.: 0.000142 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-3 (1-186)

QY 1 MetMetIlePheCyGInGlyGlnIlySylsIleAenTyArgCyS---AaenSergly 19
    |||:::|||||
DB 46 ATGCTATTTCGAGCCACGCTCAATACAGATGCTAGCTATTTGGAGAGACGAT 105
    |||:::|||||
QY 20 GluCyIleProHisCySylsIleArgIleTyraenthrArgAlaAlaIlyCySileAenIys 39
    |||:::|||||
DB 106 AATTGCGTAACCATGCTGATGATTAATACGACACAACTAAATGATCAACGAT 165
    |||:::|||||
QY 40 ThrCyAenCyTyPPro 45
    |||:::|||||
DB 166 CGGTGCAACTGTTATCCG 183
    |||:::|||||

RESULT 4
US-08-096-942-5
; Sequence 5, Application US/08096942
; Patent No. 5494895
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHIU-CHUAN S
; APPLICANT: SLAUGHTER, ROBERT S
; APPLICANT: STEVENS, SCOTT P
; TITLE OF INVENTION: SCORPION PEPIDE WITH IMMUNOSUPPRESSANT
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CATHERINE A. DOLAN, MERCK & CO., INC.
; STREET: P.O. BOX 2000, 126 LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,942
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DOLAN, CATHERINE A
; REGISTRATION NUMBER: 36502
; REFERENCE/DOCKET NUMBER: 18952
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4283
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-08-096-942-5

```

Alignment Scores:
Pred. No.: 0.000151 Length: 154
Score: 91.50 Matches: 16
Percent Similarity: 58.54% Conservative: 8
Best Local Similarity: 39.02% Mismatches: 16
Query Match: 34.40% Indels: 1
DB: 1 Gaps: 1

US-10-614-934-14 (1-45) x US-08-096-942-5 (1-154)

Qy 6 GlnGlyGlnLysLysIleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCys 25
Db 16 GAAGGTCTACCATCATCAAGTTAAATGACACTCTCCGAAACAGTGCCTCCGCCGTGC 75

Qy 26 IleArgIleTyrAsnThrArgAla---AlaLysCysIleAsnLysThrCysAsnCysTyr 44
Db 76 AAAGCTCAGTTCCGTCAGTCTGCTGCTAAATGACAAAGGTAATGCAATGCTAC 135

Qy 45 Pro 45
Db 136 CCG 138

RESULT 5
PCT-US94-08063-5
; Sequence 5, Application PC/TUS9408063
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHIU-CHUAN S
; APPLICANT: SLAUGHTER, ROBERT S
; APPLICANT: STEVENS, SCOTT P
; APPLICANT: WILLIAMSON, JOANNE M
; TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FRANK P. BIGLEY, MERCK & CO., INC.
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08063
; FILING DATE: 22-JUL-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGLEY, FRANK P.
; REGISTRATION NUMBER: 36356
; REFERENCE/DOCKET NUMBER: 18952P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-1249
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US94-08063-5

Alignment Scores:
Pred. No.: 0.000151 Length: 154
Score: 91.50 Matches: 16
Percent Similarity: 58.54% Conservative: 8

Best Local Similarity: 39.02% Mismatches: 16
Query Match: 34.40% Indels: 1
DB: 5 Gaps: 1

US-10-614-934-14 (1-45) x PCT-US94-08063-5 (1-154)

Qy 6 GlnGlyGlnLysLysIleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCys 25
Db 16 GAAGGTCTACCATCATCAAGTTAAATGACACTCTCCGAAACAGTGCCTCCGCCGTGC 75

Qy 26 IleArgIleTyrAsnThrArgAla---AlaLysCysIleAsnLysThrCysAsnCysTyr 44
Db 76 AAAGCTCAGTTCCGTCAGTCTGCTGCTAAATGACAAAGGTAATGCAATGCTAC 135

Qy 45 Pro 45
Db 136 CCG 138

RESULT 6
US-10-044-359-5
; Sequence 5, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B91367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Hottentotta judaica
; US-10-044-359-5

Alignment Scores:
Pred. No.: 0.000685 Length: 180
Score: 87.50 Matches: 18
Percent Similarity: 46.67% Conservative: 3
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 32.89% Indels: 1
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-5 (1-180)

Qy 1 MetMetIlePheCysGlnGlyGlnLysLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 46 ATGACCATATGTATTAATGCGCAAGTAGAAACAATGGAATGT---ACAGTGGCTCA 102

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaLysCysIleAsnLysThr 40
Db 103 TGTGCTTCACATGTAATAAGGTAATGAGAGTACTGCGAGAAATGCAATTAAGGAAGA 162

Qy 41 CysAsnCysTyrPro 45
Db 163 TGTGCTGCTATCCG 177

RESULT 7
US-08-096-942-2
; Sequence 2, Application US/08096942
; Patent No. 5494895
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHIU-CHUAN S

APPLICANT: SLAUGHTER, ROBERT S
APPLICANT: STEVENS, SCOTT P
APPLICANT: WILLIAMSON, JOANNE M
TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CATHERINE A. DOLAN, MERCK & CO., INC.
STREET: P.O. BOX 2000, 126 LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,942
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DOLAN, CATHERINE A
REGISTRATION NUMBER: 36502
REFERENCE/DOCKET NUMBER: 18952
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-096-942-2

Alignment Scores:
Pred. No.: 0.000545 Length: 120
Score: 86.50 Matches: 15
Percent Similarity: 58.33% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 14
Query Match: 32.52% Indels: 1
DB: 1 Gaps: 1

US-10-614-934-14 (1-45) x US-08-096-942-2 (1-120)
QY 11 ILeAnTyRrArGcYsAaAnSeRgIyGluCySIIleProHISySIIleArGIIeTyRAsn 30
Db 7 ATCAACCTTAATACCTACCTCCGAAACAGTGCCTGCCCGCGCAAGCTCACTGGGT 66

QY 31 ThrArGAla---AlaIySvCySIIleAsnLySThrCySAsnCySTyRPro 45
Db 67 CAGTCTCTGCTGCTTAATGATGATGACGTAATGCAAAATGCTACCGG 114

RESULT 8
US-10-044-359-19
Sequence 19, Application US/10044359
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: B81367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 174
TYPE: DNA
ORGANISM: Hottentotta judaica
FEATURE:
NAME/KEY: unsure
LOCATION: (9)
FEATURE:
NAME/KEY: unsure
LOCATION: (88)
US-10-044-359-19

Alignment Scores:
Pred. No.: 0.000905 Length: 174
Score: 86.50 Matches: 17
Percent Similarity: 52.27% Conservative: 6
Best Local Similarity: 38.64% Mismatches: 20
Query Match: 32.52% Indels: 1
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-19 (1-174)
QY 1 MeLMeIIePheCySgInGInLySIIleAnTyRrArGcYsAaAnSeRgIyGlu 20
Db 40 ATATATGATTTCAACGCAAGCTCAG---TTTATAGAGCTGAATGCATCATCAAGAA 96

QY 21 CySIIleProHISySIIleArGIIeTyRAsnThrArGAlaIaIySvCySIIleAsnLySThr 40
Db 97 TGTGGGCTATTGTTGAAGAAAGATTGGTGGCCAGAGAAAGTGCATTAATAAGCAA 156

QY 41 CySAsnCySTyR 44
Db 157 TGGCGTTGTAT 168

RESULT 9
US-09-857-401B-15
Sequence 15, Application US/09857401B
Patent No. 6593141
GENERAL INFORMATION:
APPLICANT: HERRMANN, RAFAEL
APPLICANT: WONG, JAMES F.
APPLICANT: LU, ALBERT L.
APPLICANT: PRESNAIL, JAMES K.
APPLICANT: LEE, JIAN-MING
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: B81102
CURRENT APPLICATION NUMBER: US/09/857,401B
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/110,590
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 180
TYPE: DNA
ORGANISM: Leiurus quinquestriatus
US-09-857-401B-15

Alignment Scores:
Pred. No.: 0.0149 Length: 180
Score: 78.00 Matches: 13
Percent Similarity: 56.67% Conservative: 4
Best Local Similarity: 43.33% Mismatches: 13
Query Match: 29.32% Indels: 0
DB: 4 Gaps: 0

US-10-614-934-14 (1-45) x US-09-857-401B-15 (1-180)
QY 15 CySAsnAnSeRgIyGluCySIIleProHISySIIleArGIIeTyRAsnThrArGAlaIa 34

```

Db      85  TCGAGTCATGATCAATGTTGTTGTCTCAAACTGTATATAAAGCTCAATGCA 144
      |||::|||:::|||||:::|||||
Qy      35  LysCysIleAsnLysThrCysAsnCysTyr 44
      |||:::|||||:::|||||
Db      145  AAGTGTATGATATAATAATGCCGCTGTAT 174
      |||:::|||||:::|||||

```

RESULT 10

```

US-09-857-401B-11
; Sequence 11, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESMAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Leiurus quinquestriatus
US-09-857-401B-11

```

Alignment Scores:

```

Pred. No.: 0.0161 Length: 150
Score: 77.00 Matches: 13
Percent Similarity: 50.00% Conservative: 2
Best Local Similarity: 43.33% Mismatches: 15
Query Match: 28.95% Indels: 0
DB: 4 Gaps: 0

```

```

US-10-614-934-14 (1-45) x US-09-857-401B-11 (1-150)

```

```

Qy      15  CysAsnAsnSerGlyLysCysIleProHisCysIleArgLysThrArgAlaAla 34
      |||:::|||||:::|||||
Db      58  TGTACTACATCAATGAATGTTGTCGTTGTGAGACATGTATATAGCCACAGAGA 117
      |||:::|||||:::|||||
Qy      35  LysCysIleAsnLysThrCysAsnCysTyr 44
      |||:::|||||:::|||||
Db      118  AAGTCATGAAATGGAAATGCCGCTGTAT 147
      |||:::|||||:::|||||

```

RESULT 11

```

US-10-044-359-15
; Sequence 15, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-15

```

```

Alignment Scores:
Pred. No.: 0.0382 Length: 176
Score: 75.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 28.20% Indels: 0
DB: 4 Gaps: 0

```

```

US-10-614-934-14 (1-45) x US-10-044-359-15 (1-176)

```

```

Qy      11  IleAsnTyrArgCysAsnAsnSerGlyLysCysIleProHisCysIleArgLysThrAsn 30
      |||:::|||||:::|||||
Db      73  ATGACGTGAAGATGATGCTCTGCTGATGTTGGAACTTGCAAGAAAGTAACAGCA 132
      |||:::|||||:::|||||
Qy      31  ThrArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
      |||:::|||||:::|||||
Db      133  TCGAGCAAGAAAGTCCAGAAATACCAATGCTGTTAT 174
      |||:::|||||:::|||||

```

RESULT 12

```

US-09-857-401B-1
; Sequence 1, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESMAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Leiurus quinquestriatus
US-09-857-401B-1

```

```

Alignment Scores:
Pred. No.: 0.0736 Length: 177
Score: 73.00 Matches: 14
Percent Similarity: 45.00% Conservative: 4
Best Local Similarity: 35.00% Mismatches: 22
Query Match: 27.44% Indels: 0
DB: 4 Gaps: 0

```

```

US-10-614-934-14 (1-45) x US-09-857-401B-1 (1-177)

```

```

Qy      5  CysGlnGlyGlnLysLysIleAsnTyrArgCysAsnAsnSerGlyLysCysIleProHis 24
      |||:::|||||:::|||||
Db      55  TGTAGTGAAGCTGAGCTCATGACCTAGAGATGTTTGCATCTCGTAATGTTGGAGACT 114
      |||:::|||||:::|||||
Qy      25  CysIleArgLysThrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
      |||:::|||||:::|||||
Db      115  TCGAGAAAGTAACAGATCGGACACAGAAATGCCAGAAATATCAATGTCGCTAT 174
      |||:::|||||:::|||||

```

RESULT 13

```

US-10-044-359-17
; Sequence 17, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416

```

```

; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-17

Alignment Scores:
Pred. No.: 0.141 Length: 177
Score: 71.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 26.69% Indels: 0
DB: 4 Gaps: 0

US-10-614-934-14 (1-45) x US-10-044-359-17 (1-177)
Qy 11 leasntYrargCysaAsnSerglyGluCysileProHieCysileArgileTyraSn 30
Db 73 ATGACGCTAAATATATTCTCTCAAGAAATGTTGGATGCTGTGTAATAAAGTAACTGGA 132
Qy 31 ThrArgAlaAlaIySvSileAsnLySthrCysaSnCysTyR 44
Db 133 CGGTTCAAGGAATAATGCGCAATTAACAATGTCGCTGTAT 174

RESULT 14
PCT-US94-08063-2
; Sequence 2, Application PC/TUS9408063
; GENERAL INFORMATION:
; APPLICANT: GARCIA, MARIA L
; APPLICANT: KOO, GLORIA C
; APPLICANT: LEONARD, REID J
; APPLICANT: LIN, CHIU-CHUAN S
; APPLICANT: SLAUGHTER, ROBERT S
; APPLICANT: STEVENS, SCOTT P
; APPLICANT: WILLIAMSON, JOANNE M
; TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: FRANK P. BIGLEY, MERCK & CO., INC.
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08063
; FILING DATE: 22-JUL-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGLEY, FRANK P.
; REGISTRATION NUMBER: 36356
; REFERENCE/DOCKET NUMBER: 18952P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-1249
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-08063-2

Alignment Scores:
Pred. No.: 0.201 Length: 127
Score: 68.50 Matches: 15
Percent Similarity: 53.85% Conservative: 6
Best Local Similarity: 38.46% Mismatches: 14
Query Match: 25.75% Indels: 4
DB: 5 Gaps: 1

US-10-614-934-14 (1-45) x PCT-US94-08063-2 (1-127)
Qy 11 leasntYrargCysaAsnSerglyGluCysileProHieCysileArgileTyraSn 30
Db 7 ATGACGCTAAATATGCACTCTCCGAAACAGTCGCGCCGCGCAAGCTCACTGCGT 66
Qy 31 ThrArgAla-----AlaIySvSileAsnLySthrCysaSnCysTyRPro 45
Db 67 CAGTCTGCTGCTGCTAAATGCTAAATGCAATGCAATGCAATGCTACCG 121

RESULT 15
US-09-949-016-11817
; Sequence 11817, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11817
; LENGTH: 124700
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11817

Alignment Scores:
Pred. No.: 2.41e+03 Length: 124700
Score: 68.50 Matches: 15
Percent Similarity: 38.98% Conservative: 8
Best Local Similarity: 25.42% Mismatches: 19
Query Match: 25.75% Indels: 17
DB: 4 Gaps: 1

US-10-614-934-14 (1-45) x US-09-949-016-11817 (1-124700)
Qy 4 PhnCysglInglyGlnIySvSileAsntYrargCysaSnSerglyGlu----- 20
Db 91091 TTCTGTGAAATTTCCAGGTCGAGATCATCTTAACAGTACACAGCAATCATCAT 91150
Qy 21 -----CysileProHieCysile 26
Db 91151 CCTCCATCCAGATTAAACAATGTTGATCATTTGCTTTCAGCATTTGTTG 91210
Qy 27 ArgIleTyraSnThrArgAlaAlaIySvSileAsnLySthrCysaSnCysTyRPro 45
Db 91211 TTGACTTATGTAATAACCACTACAGGTGATCATCTTCGCAACTGTATCC 91267

Search completed: August 19, 2005, 10:23:20
Job time : 144 secs

```


Fri Aug 19 10:52:13 2005

us-10-614-934-14.rml

Page 7

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using.frame_plus.p2n model

Run on: August 19, 2005, 03:05:35 ; Search time 622 Seconds

(without alignments)
470.034 Million cell updates/sec

Title: US-10-614-934-14

Perfect score: 266

Sequence: 1 MMIFCQCKKINRCNNGE.....IRIYNTRAKKINCKNCYP 45

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 10.0, Fgapext 0.5
Delop 6.0, Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODUL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USP70_sepol_p/US10614934/runcat_17082005_181355_22021/app.query.fasta.1.199
-DB=Published_Applications_NA -Qfmt=faeap -Sufix=rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=spc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USR=US10614934.ccn 1.1.723 @runcat_17082005_181355_22021
-NCPU=6 -ICPU=3 -NO MMAP -LARGEOUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	266	100.0	138	21	US-10-614-934-13	Sequence 13, Appl
2	101	38.0	114	21	US-10-614-934-9	Sequence 9, Appl
3	92.5	34.8	186	13	US-10-044-359-3	Sequence 3, Appl
4	87.5	32.9	180	13	US-10-044-359-5	Sequence 5, Appl
5	86.5	32.5	174	13	US-10-044-359-19	Sequence 19, Appl
6	79.5	29.9	231	9	US-09-728-446-356	Sequence 356, App
7	78	29.3	180	21	US-10-614-934-15	Sequence 15, Appl
8	77	28.9	150	21	US-10-614-934-11	Sequence 11, Appl
9	75	28.2	176	13	US-10-044-359-15	Sequence 15, Appl
10	73	27.4	177	21	US-10-614-934-1	Sequence 1, Appl
11	71.5	26.9	905	18	US-10-425-114-17548	Sequence 17548, A
12	71.5	26.9	1405	18	US-10-425-114-23882	Sequence 23882, A
13	71.5	26.9	1770	20	US-10-425-115-38932	Sequence 38932, A
14	71.5	26.9	2525	20	US-10-425-115-38929	Sequence 38929, A
15	71	26.7	177	13	US-10-044-359-17	Sequence 17, Appl
16	69.5	26.1	3846	19	US-10-437-963-33842	Sequence 33842, A
17	68.5	25.8	73100	19	US-10-319-914-11	Sequence 11, Appl
18	68	25.6	350570	20	US-10-417-375-146	Sequence 146, App
19	66.5	25.0	83009	20	US-10-417-375-143	Sequence 143, App
20	66	24.8	204	21	US-10-721-793-131	Sequence 131, App
21	66	24.8	323	21	US-10-721-793-129	Sequence 129, App
22	66	24.8	626	13	US-10-027-632-281127	Sequence 281127, A
23	66	24.8	377	20	US-10-027-632-281127	Sequence 281127, A
24	65.5	24.6	377	20	US-10-425-115-166413	Sequence 166413, A
25	65	24.4	288	19	US-10-437-963-57403	Sequence 57403, A
26	65	24.4	316	19	US-10-437-963-11987	Sequence 11987, A
27	64	24.1	2185	17	US-10-104-047-556	Sequence 556, App
28	64	24.1	2422	19	US-10-437-963-4897	Sequence 4897, App
29	64	24.1	42360	19	US-10-367-094-148	Sequence 148, App
30	64	24.1	143306	9	US-09-729-920-3	Sequence 3, Appl
31	64	24.1	143306	20	US-10-887-932-3	Sequence 3, Appl
32	63.5	23.9	3552	17	US-10-369-493-24016	Sequence 24016, A
33	63.5	23.9	3543	18	US-10-425-114-26499	Sequence 26499, A
34	63.5	23.9	50000	21	US-10-706-635-24	Sequence 24, Appl
35	63.5	23.9	366710	20	US-10-719-993-5792	Sequence 5792, App
36	63	23.7	533	16	US-10-029-386-5501	Sequence 5501, App
37	63	23.7	671	13	US-10-027-632-15307	Sequence 15307, A
38	63	23.7	671	13	US-10-027-632-15307	Sequence 15307, A
39	63	23.7	671	17	US-10-027-632-15307	Sequence 15307, A
40	63	23.7	671	17	US-10-027-632-15308	Sequence 15308, A
41	63	23.7	891	14	US-09-810-836B-7	Sequence 7, Appl
42	63	23.7	891	14	US-10-286-264-53	Sequence 63, Appl
43	63	23.7	891	15	US-10-295-403-21	Sequence 21, Appl
44	63	23.7	891	17	US-10-225-066A-559	Sequence 559, App
45	63	23.7	891	17	US-10-374-780A-2437	Sequence 2437, App

ALIGNMENTS

RESULT 1
US-10-614-934-13
; Sequence 13, Application US/10614934
; Publication No. US20050042717A1
GENERAL INFORMATION:
APPLICANT: HERRMANN, RAFAEL
APPLICANT: WONG, JAMES F.
APPLICANT: LU, ALBERT L.
APPLICANT: PRESNALL, JAMES K.
APPLICANT: LEE, JIAN-MING
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: B01102
CURRENT APPLICATION NUMBER: US/10/614,934
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/857,401
PRIOR FILING DATE: 2001-06-01

```

; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 138
; TYPE: DNA
; ORGANISM: Leirurus quinquestrictus
US-10-614-934-13

Alignment Scores:
Pred. No.: 1,14e-27 Length: 138
Score: 266.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-13 (1-138)

Qy 1 MetNcIlePheCySGInGlyGlnIylsIleAsnTyRgCYsAsnAsnSerGlyGlu 20
Db 1 ATGATGATTTCTGCGAAGCCAGAAAATAATTTCATGTAAATATAGCGGTGAG 60

Qy 21 CysIleProHisCySIIeArgIleTyRAsnThrArgAlaAlaIylsCySIIeAsnIylsThr 40
Db 61 TGTATTCCACATGTGATCAGATATATATACACACAGACGAGAAAGTGTATTAATAAACA 120

Qy 41 CysAsnCySTyRPro 45
Db 121 TGCATTTGTATCCA 135

RESULT 2
US-10-614-934-9
; Sequence 9, Application US/10614934
; Publication No. US20050042717A1
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/10/614,934
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/857,401
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Leirurus quinquestrictus
US-10-614-934-9

Alignment Scores:
Pred. No.: 5.05e-05 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-9 (1-114)

Qy 12 AsnTyRgCYsAsnAsnSerGlyGluCySIIeProHisCySIIeArgIleTyRAsnThr 31
Db 10 AATGTGCGCGTGCAGAAATTTCTGACAAATGTGTCACAGTTTGCATTAATAAAGTAATAT 69

Qy 32 ArgAlaAlaIylsCySIIeAsnIylsThrCyAsnCySTyRPro 45
```

```

Db 70 AATGCGGAAAGTGTGTAATGACCAATGTATTGTATCCA 111

RESULT 3
US-10-044-359-3
; Sequence 3, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Hottentotca judaica
US-10-044-359-3

Alignment Scores:
Pred. No.: 0.00141 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 13 Gaps: 1

US-10-614-934-14 (1-45) x US-10-044-359-3 (1-186)

Qy 1 MetNcIlePheCySGInGlyGlnIylsIleAsnTyRgCYs---AsnAsnSerGly 19
Db 46 ATGTTATTTCGAGCCAGCTCAATACGAGTTGATGTAACGTGTATGGAGAGACAGAT 105

Qy 20 GlucySIIeProHisCySIIeArgIleTyRAsnThrArgAlaAlaIylsCySIIeAsnIyls 39
Db 106 AATGCGTAAACCATCTATGATTAATACGGCACCACTAAACTAAATGATCAACGAT 165

Qy 40 ThrCyAsnCySTyRPro 45
Db 166 CGTGCACACTGTATCCG 183

RESULT 4
US-10-044-359-5
; Sequence 5, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Hottentotca judaica
US-10-044-359-5
```

Alignment Scores:	
Pred. No.:	0.0066
Score:	87.50
Percent Similarity:	46.67%
Best Local Similarity:	40.00%
Query Match:	32.89%
DB:	13
Length:	180
Matches:	18
Conservative:	3
Mismatches:	23
Indels:	1
Gaps:	1

US-10-614-934-14 (1-45) X US-10-044-359-5 (1-180)

Oy		1	M e M e r t l e p h e c y s i n g i v g i n y l s i l l e a n T y R A C G S a n a n s e c I G l u	20
			: :	
D b		46	A T A C C C T A T A G T T A T T A T T C C A G A G A A A C A A A T G C A A T G T - - - A C A G G C G C T C A	102
Oy		21	C y e l l e r o h i s c Y s i l l e a r g i l e t y r a a n t t o r a g A l a a l a y s C y e l l e a s n l y e t h r	40
			: :	
D b		103	T G T G C T T C A A C A C T A A A A A C A G T A A T A G A A G T A G C T C A G S A A A T G C A T T A T A G A A G A	162
Oy		41	C y e a s n C y s T y P r o	45
			: :	
D b		163	T G T G T G C T A T C C G	177

RESULT 5

```

US-10-044-359-19
? Sequence 19, Application US/10044359
? Publication No. US20020160454A1
?
? GENERAL INFORMATION:
? APPLICANT: Heirman, Rafael
? APPLICANT: Wong, James F.
? APPLICANT: Lee, Jian-Ming
? TITLE OF INVENTION: SCORPTION TOXINS
? FILE REFERENCE: BB1367 US NA
? CURRENT APPLICATION NUMBER: US/10/044,359
? CURRENT FILING DATE: 2002-01-11
? PRIOR APPLICATION NUMBER: 09/599,416
? PRIOR FILING DATE: 2000-06-22
? PRIOR APPLICATION NUMBER: 60/140,227
? PRIOR FILING DATE: 1999-06-22
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: Microsoft Office 97
? SEQ ID NO 19
?
? LENGTH: 174
?
? TYPE: DNA
?
? ORGANISM: Hottentotta judaica
?
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (9)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (88)
?
? US-10-044-359-19

```

Alignment Scores:	
Pred. No.:	0.00869
Score:	86.50
Percent Similarity:	52.27%
Best Local Similarity:	38.64%
Query Match:	32.52%
DB:	13
Length:	174
Matches:	17
Conservative:	6
Mismatches:	20
Indels:	1
Gaps:	1

US-10-614-934-14 (1-45) X US-10-044-359-19 (1-174)

[illegible]

RESULT 6
US-09-728-446-356

```

? Sequence 356, Application US/09728446
? Patent No. US20020081668A1
? GENERAL INFORMATION:
? APPLICANT: Friedrich, Glenn
? APPLICANT: Sands, Arthur T.
? APPLICANT: Zambrowicz, Brian
? TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
? TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
? FILE REFERENCE: LEX-0101-USA
? CURRENT APPLICATION NUMBER: US/09/728,446
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/168,270
? PRIOR FILING DATE: 1999-12-01
? NUMBER OF SEQ ID NOS: 1461
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 356
? LENGTH: 231
? TYPE: DNA
? ORGANISM: Mus musculus
? US-09-728-446-356

```

Alignment Scores:	
Pred. No.:	0.115
Score:	79.50
Percent Similarity:	47.73%
Best Local Similarity:	36.36%
Query Match:	29.89%
DB:	9
Length:	23
Matches:	16
Conservative:	5
Mismatches:	20
Indels:	1
Gaps:	1

US-10-614-934-14 (1-45) X US-09-728-446-356 (1-231)

Oy PheCysGlnGlnGlnLysLysIleAsnTYrArgCysAsnAsnSer-----GlyGlu 20
 Db TTTCTCTCCAGGAGAGAAAGCCCTCTCTTGAAATATTAATATATCAAAAAATTTGGGGTC 143
 Oy CysIleProHisCysIleArgIleTYrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 Db TGTTCCTCCATTTGTGTGTGGAGATATATATCCATCTTCTATTAATTGGCCAACTAGTAAT 203
 Oy CysAsnCysTYr 44
 Db TGTAAATGGCTT 215

RESULT 7

```

US-10-614-934-15
? Sequence 15, Application US/10614934
? Publication No. US20050042717A1
? GENERAL INFORMATION:
? APPLICANT: HERPMANN, RAFAEL
? APPLICANT: WONG, JAMES F.
? APPLICANT: LU, ALBERT L.
? APPLICANT: PRESNALL, JAMES K.
? APPLICANT: LEE, JIAN-JING
? TITLE OF INVENTION: SCORPION TOXINS
? FILE REFERENCE: BH1102
? CURRENT APPLICATION NUMBER: US/10/614,934
? CURRENT FILING DATE: 2003-07-08
? PRIOR APPLICATION NUMBER: US/09/857,401
? PRIOR FILING DATE: 2001-06-01
? PRIOR APPLICATION NUMBER: 60/110,590
? PRIOR FILING DATE: 1998-12-02
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: Microsoft Office 97
? SEQ ID NO 15
? LENGTH: 180
? TYPE: DNA
? ORGANISM: Leiurus quinquestriatus
US-10-614-934-15
Alignment Scores:

```

Pred. No.: 0.135 Length: 180
 Score: 78.00 Matches: 13
 Percent Similarity: 56.67% Conservative: 4
 Best Local Similarity: 43.33% Mismatches: 13
 Query Match: 29.32% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-15 (1-180)

QY 15 CysAenAnserGlyCysIleProHisCysIleArgIleTyrAenThrArgAlaAla 34
 Db 85 TGCAGTCATCTGATCATCTGTTGGTTGTTCTCAAACTGTATTAACACCTCATGCA 144

QY 35 LysCysIleAenLysThrCysAenCysTyr 44
 Db 145 AAGTGATGATTAATTAATGCCGCTGTAT 174

RESULT 8

US-10-614-934-11
 ; Sequence 11, Application US/10614934
 ; Publication No. US20050042717A1
 ; GENERAL INFORMATION:

APPLICANT: HERMANN, RAFAEL
 APPLICANT: WONG, JAMES F.
 APPLICANT: LU, ALBERT L.
 APPLICANT: PRESNAIL, JAMES K.
 APPLICANT: LEE, JIAN-MING
 TITLE OF INVENTION: SCORPION TOXINS
 FILE REFERENCE: BB1102
 CURRENT APPLICATION NUMBER: US/10/614,934
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: US/09/857,401
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: 60/110,590
 PRIOR FILING DATE: 1998-12-02
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 11
 LENGTH: 150
 TYPE: DNA
 ORGANISM: Leiurus quinquestriatus
 US-10-614-934-11

Alignment Scores:
 Pred. No.: 0.146 Length: 150
 Score: 77.00 Matches: 13
 Percent Similarity: 50.00% Conservative: 2
 Best Local Similarity: 43.33% Mismatches: 15
 Query Match: 28.95% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-11 (1-150)

QY 15 CysAenAnserGlyCysIleProHisCysIleArgIleTyrAenThrArgAlaAla 34
 Db 58 TGTACTACATCTAAAGATGTTGTCGTGTGAGACATTGTATTAAGACCAAGAGGA 117

QY 35 LysCysIleAenLysThrCysAenCysTyr 44
 Db 118 AAGTGATGATTAATTAATGCCGCTGTAT 147

RESULT 9

US-10-044-359-15
 ; Sequence 15, Application US/10044359
 ; Publication No. US20020160454A1
 ; GENERAL INFORMATION:

APPLICANT: Herrman, Rafael
 APPLICANT: Wong, James F.
 APPLICANT: Lee, Jian-Ming
 TITLE OF INVENTION: SCORPION TOXINS
 FILE REFERENCE: BB1367 US NA
 CURRENT APPLICATION NUMBER: US/10/044,359
 CURRENT FILING DATE: 2002-01-11

PRIOR APPLICATION NUMBER: 09/599,416
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 60/140,227
 PRIOR FILING DATE: 1999-06-22
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 15
 LENGTH: 176
 TYPE: DNA
 ORGANISM: Hottentotta judaica
 US-10-044-359-15

QY 11 IleAsnTyrArgCysAenAnserGlyCysIleProHisCysIleArgIleTyrAsn 30
 Db 73 ATAGACGTAAAGATGATGCTCTCGTAATGTTGGAAAGCTTCAGAAAAGTAACAGCA 132

QY 31 ThrArgAlaAlaLysCysIleAenLysThrCysAenCysTyr 44
 Db 133 TCGAGACAGAAAGTCCAGAAATTAACCATGTGCTGTAT 174

RESULT 10

US-10-614-934-1
 ; Sequence 1, Application US/10614934
 ; Publication No. US20050042717A1
 ; GENERAL INFORMATION:

APPLICANT: HERMANN, RAFAEL
 APPLICANT: WONG, JAMES F.
 APPLICANT: LU, ALBERT L.
 APPLICANT: PRESNAIL, JAMES K.
 APPLICANT: LEE, JIAN-MING
 TITLE OF INVENTION: SCORPION TOXINS
 FILE REFERENCE: BB1102
 CURRENT APPLICATION NUMBER: US/10/614,934
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: US/09/857,401
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: 60/110,590
 PRIOR FILING DATE: 1998-12-02
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 1
 LENGTH: 177
 TYPE: DNA
 ORGANISM: Leiurus quinquestriatus
 US-10-614-934-1

Alignment Scores:
 Pred. No.: 0.645 Length: 177
 Score: 73.00 Matches: 14
 Percent Similarity: 45.00% Conservative: 4
 Best Local Similarity: 35.00% Mismatches: 22
 Query Match: 27.44% Indels: 0
 DB: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-1 (1-177)

QY 5 CysGlnGlyGlnLysLysIleAsnTyrArgCysAenAnserGlyCysIleProHis 24
 Db 55 TGTAGTGAAGCTGAGCTCATGAGAGATGTTTTCATCTCGTGAATGTTGGAAAGCT 114

QY 25 CysIleArgIleTyrAenThrArgAlaAlaLysCysIleAenLysThrCysAenCysTyr 44
 Db 115 TGCAGAAAGTAACAGATGCGGACAGAAAGTAATGCCAGATTAATCATATGCTGCTAT 174

```

: FEATURE:
: OTHER INFORMATION: Clone ID: LIB3606-012-B7_FLI
US-10-425-114-23882

Alignment Scores:
Pred. No.: 14.9 Length: 1405
Score: 71.50 Matches: 15
Percent Similarity: 34.92% Conservative: 7
Best Local Similarity: 23.81% Mismatches: 18
Query Match: 26.88% Indels: 23
DB: 18 Gaps: 1

US-10-614-934-14 (1-45) x US-10-425-114-23882 (1-1405)

QY 5 CysGlnGlyGlnIlyblyslleAsnTYrRGcysaAnaSergIyGlucyslleProHis 24
Db 826 TGCACAGGCCAGAGAGAGATTGATTTCTGTCAACCCACAGTGGAGCTCAATTGTGCAC 885
QY 25 Cys----- 25

Db 886 TGCTGCGGCAAGTTGTCAAAGGCTCCCCAGAAAATGATCAACCGGCTCCAGTGGCCGA 945
QY 26 -----1leatgiletyrAsnThrArgAlaIalalyCyslleAsnlysthrCys 41
Db 946 GAACATCTCTCCGTCAATGATGTCAAGACATTTCAACAGATGTTCCACGAGCGTGC 1005
QY 42 AsnCyStyr 44
Db 1006 GGATGCCAT 1014

RESULT 13
US-10-425-115-38932
: Sequence 38932, Application US/10425115
: Publication No. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yinhua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(5322)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 369326
: SEQ ID NO 38932
: LENGTH: 1770
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: MFT4577_135507C.1
US-10-425-115-38932

Alignment Scores:
Pred. No.: 20.1 Length: 1770
Score: 71.50 Matches: 15
Percent Similarity: 34.92% Conservative: 7
Best Local Similarity: 23.81% Mismatches: 18
Query Match: 26.88% Indels: 23
DB: 20 Gaps: 1

US-10-614-934-14 (1-45) x US-10-425-115-38932 (1-1770)

QY 5 CysGlnGlyGlnIlyblyslleAsnTYrRGcysaAnaSergIyGlucyslleProHis 24
Db 1143 TGCCAGAGCCAGAGAGAGATTGATTTCTGTCAACCCACAGTGGAGCTCAATTGTGCAC 1202
QY 25 Cys----- 25
Db 1203 TGCTGCGGCAAGTTGTCAAAGGCTCCCCAGAAAATGATCAACCGGCTCCAGTGGCCGA 1262
QY 26 -----1leatgiletyrAsnThrArgAlaIalalyCyslleAsnlysthrCys 41

```

